Perfect score:

Sequence:

OM nucleic

ou:

Run

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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HSJ1056K3 143981 bp DNA linear PRI 04-APR-2001 Human DNA sequence from clone RPS-1050K3 on chromosome 20. Contains part of the EYA2 gene for eyes absent (Drosophila) homolog 2, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) pseudogene, an RPL27A (665 ribosomal protein L27A) pseudogene, ESTS, STSs and
AL121776 Human DNA
AL662786 Mus muscu
AJ336191 Homo sap1
AJ331419 Homo sap1
AJ34149 Homo sap1
AC106623 Rattus no
AC021089 Homo sap1
AC004257 Oryza sat
AC06570 Rattus no
AC021791 Caenorhab
AC015769 Homo sap1
AC015769 Homo sap1
AC017751 Mus muscu
AC077751 Mus muscu
AC077755 Mus muscu
AC077755 Mus muscu
AC077755 Mus muscu
AC077769 Homo sap1
AC107297 Homo sap1
AC107297 Homo sap1
AC007609 Homo sap1
AC007609 Homo sap1
AC013537 Trypanoso
AP0043197 Aryza sat
AC007609 Homo sap1
AC013537 Trypanoso
AC077155 Drosoph11
AC013537 Trypanoso
AC077155 Drosoph11
AC013537 Trypanoso
AC077155 Drosoph11
AC013537 Trypanoso
                                                                                                                                                                                                                                                                                                                                         74 Homo sapi
51 Mus muscu
25 Mus muscu
27 Schizosac
47 Drosophil
Caenorhabdi
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Submitted (03-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (03-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
reguests: User Sanger Sa
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Homo sapi
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Drosophil
Thermopla
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musco
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                                               HSA336359
HSA336191
HSA334149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSs, complete sequence.
AL121776
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63528
100511
156929
196057
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27777
42844
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56780
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  Peck, A.
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  \begin{array}{c} 2.1 \\ 2.1 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\ 3.2 \\
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HSJ1050K3
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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       0000000
                                                                                                                                                              July 25, 2002, 05:37:18; Search time 3312.9 Seconds (without alignments) 132.650 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3595312
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                                                   1 atgtcgggcggtggaaatatc 21
                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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em_htg_other:*
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seq length: 200000000
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                                                                                                                                                                                                                                                                US-09-235-416-3
21
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Match Length DB
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9b_htg:*
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9b_on:*
9b_pat:*
9b_ph:*
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Score

Result ġ

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http://www.sanger.com.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-1050K3 The true right end of clone RP11.32151 is at 58476 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1050K3 is from the library RPCI-5 constructed by the group of Pieter de Jong. For
                                                                                   corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "LIMC4 repeat: matches 7626. .7750 of consensus"
i002. .5192
note="MIR repeat: matches 52. .248 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L1MC4 repeat: matches 7750. .7977 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134. .175
/note="L2 repeat: matches 2709. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 2669. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER46A repeat: matches 2. .235 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1387. .1679
/note="AluSx repeat: matches 1. .294 of consensus"
2480. .2676
/note="MIR repeat: matches 41. .262 of consensus"
complement(2633. .2991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544. .4059
note="MLTIF repeat: matches 1. .541 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .260 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .246 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 1. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote="14 copies 2 mer tt 89% conserved" 2926. 3557
Anote="match: GSS: Em:AQ423175" 2930. 3460
Anote="match: GSS: Em:AQ423187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omplement(2033. .2991)
note="match: GSS: Em:AQ017978"
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note="match: GSS: Em:AQ787200"
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'note="MIR repeat: matches 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109. .3326 _
note="MIR repeat: matches 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further details see
http://www.chorl.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .143981
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RR5-1050K3"
/clone="RR5-11b="RPCI-5"
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/note="L2 rep
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12718. .13297
12718. .15297 /note="AluSp repeat: matches 140. .298 of consensus" /note="MIR repeat: matches 103, .241 of consensus" 11776, .11966 /note="MER58A repeat: matches 6, .224 of consensus" 12110, .12326 7395. 7610
Anote="AluJo repeat: matches 95. .310 of consensus" 7809. .7952
Anote="MIR repeat: matches 28. .184 of consensus" 7953. .8262
Anote="MILS repeat: matches 1. .312 of consensus" 7005="MILS repeat: matches 1. .312 of consensus" 8263. .8288
Anote="MIR repeat: matches 184. .207 of consensus" /note="AluJb repeat: matches 11. .295 of consensus" 10370. .10506 /note="1.2 repeat: matches 2621. .2689 of consensus" complement(16294. .16547) .2740 of consensus" .2374 of consensus" .2709 of consensus" /note="MIR repeat: matches 63. 245 of consensus" 6951. 7253 /note="AluJo repeat: matches 1. 305 of consensus" 7254. 7265 /note="MIR repeat: matches 245. 256 of consensus" 7395. 7610 18770. .18941 /note="MER20 repeat: matches 3. .184 of consensus" 19066. .19554 8596. .8676 Toto="MIR repeat: matches 109. .199 of consensus" 9736. .9877 Toto="MIR repeat: matches 109. .255 of consensus" 10029. .10325 .164 of consensus" 18336. 18486 Note="MIR repeat: matches 98. 261 of consensus" /note="MIR repeat: matches 53. .192 of consensus" 6517. .6723 .215 of consensus" .2750 of /note="match: GSS: Em:B14853"
17097. 17504
17097. 17504
17149. 17400
/note="L2 repeat: matches 2468...
17433. 17605
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17676. 17729
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HSA336359 737 bp DNA linear PRI 01-OCT-2001
Homo sapiens genomic sequence surrounding NotI site, clone
HSJ-CB3RS.
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Kutsenko, A. S., Gizatullin, R. Z., Al-Amin, A. N., Wang, F., Podowski, R. M., Matushkin, Y. G., Kvasha, S. M., Gyanchandani, A., Muravenko, O. V., Protopopov, A. I., Kashuba, V. I., Kisselev, L. L.,
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  Consensus quality: 202716 bases at least Q40 Consensus quality: 203013 bases at least Q30 Consensus quality: 203237 bases at least Q30 Insert size: 203467; sum-of-contigs Insert size: 198131; 4.7% error; agarcose-fp Quality coverage: 10.99x in Q20 bases; sum-of-contigs quality coverage: 11.59x in Q20 bases; agarose-fp
                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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/note="assembly_fragment:02278
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-340010"
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RP23-340010, *** SEQUENCING IN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On bec 1B, 2001 this sequence version replaced gi:17736652.
--------------- Genome Center
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                .6142 of consensus"
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                                                                                                                                                                                              /2255. .23043
//Orde="Mirror repeat: matches 180. .250 of consensus" 22535. .23043
//Orde="Mirror repeat: matches 7. .497 of consensus" 23092. .23510
//Orde="match: GSS: Em:AQ306389"
//Orde="LiPAl3 repeat: matches 5573. .6142 of consensus complement(4352. .24917)
//Orde="match: GSS: Em:AQ667419"
//Orde="matches 31. .218 of consensus"
//Orde="Mirror repeat: matches 32. .249 of consensus"
//Orde="Mirror repeat: matches 32. .249 of consensus"
//Orde="Mirror repeat: matches 32. .249 of consensus"
21031. .21255
/note="MEFSBA repeat: matches 1. .224 of consensus" 21526. .21609
21702. .21609
21723. .21925
/note="MLF11 repeat: matches 322. .410 of consensus" 21723. .21925
/note="MLF11 repeat: matches 19. .261 of consensus" 21942. .22258
22267. .22337
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/25803. .26008

/note="MER58A repeat: matches 9. .224 of consensus"

26250. .26541

/note="Aluxx repeat: matches 1. .301 of consensus"

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/note="LimA5" repeat: matches 5469. .6149 of consensus"
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Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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Mus musculus chromosome 11 clone F
PROGRESS ***, in unordered pieces.
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Web site: http://www.sanger.ac.uk
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AL662786.2 GI:17903997
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Podowski, R.M., Matushkin, Y.G., Kvasha, S.M., Gyanchandani, A.,
Muravenko, O.V., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L.,
Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
Analysis of Norl flanking sequences: a new tool for gene discovery
and verification of the human genome
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Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Rarolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Analysis of Noti flanking sequences: a new tool for gene discovery and verification of the human genome
                                                                                    Direct Subinsion
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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AJ336191.1 GI:15880609
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11arity 90.0%; Pred. No. 1e+03;
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/organism="Homo sapiens"
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a 228 c 229 g 154
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Zabarovsky, E.R.
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Zabarovsky, E.R.
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RESULT

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AC106623

Rattus norvegicus clone CH230-224B2, *** SEQUENCING IN PROGRESS

***, 46 unordered pieces.

AC106623 1 GI:18139147
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Homo sapiens genomic sequence surrounding NotI site, clone HSL-DL/Rs.
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I bases 1 to 792)
Kutsenko,A.S., Gizalliin,R.Z., Al-Amin,A.N., Wang,F.,
Fodowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Amsserman,W., Wahlestedt,C. and Zabarovsky,E.R.
Analysis of Notr flanking sequences: a new tool for gene discovery and verification of the human genome
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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/organism="Homo sapiens"
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Zabarovsky, E.R.
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Rattus norvegicus
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Matches 18; Conservative
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Hollins, B., Homei, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kalisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kurstovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Louiseged, H., Lozado, R.J., Lu, X., Luder, M., Leuder, R., Luna, R., Martinez, E., Massey, E., Marhin, R., Martindale, A., Luder, R., Martinez, E., Massey, E., Mawhiney, E., McIeod, M.P., Meador, M., Medi, G., Metzker, M., Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Ned, D., Newtson, J., Newtson, N., Nquyen, N., Nquyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Put. L., Quiles, M., Ren, Y., Rives, M., Rojado, R., Pace, A., Payton, B., Sodergen, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmanl, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Walliqans, G., Williams, G., Walliamson, A., Walliams, G., Williamson, A., Walliams, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Consensus quality: 70064 bases at least Q30
Consensus quality: 75160 bases at least Q30
Estimated insert size: 56201; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 0.6x in Q20 bases; sum-of-contigs estimation
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Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 97446 bases at least Q40
Consensus quality: 96488 bases at least Q30
Consensus quality: 96488 bases at least Q30
Consensus quality: 9816 bases at least Q30
Estimated insert size: 106000; agarose-fp estimation
Betimated insert size: 10612 sum-of-contigs estimation
Quality coverage: 6.37 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.37 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "vorking draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 4526 4625; contig of 4525 bp in length
* 4526 21040; contig of 16415 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               100912 bp DNA linear HTG 25-APR-2001
Homo sapiens chromosome 16 clone CTD-2264D9, WORKING DRAFT
SEQUENCE, 11 ordered pleces.
AC021089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Apr 25, 2001 this sequence version replaced gi:9964760.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I ( pases 1 to 100912)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                              Length 88941;
                                                                                                                                                                                       4533 others
                                                                                                                                                                                                                                                                                                        Indels
  12 86241: gap of unknown length
12 87699: contig of 1458 bp in length
10 87799: gap of unknown length
10 88941: contig of 1142 bp in length.
10 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACÔ21089
ACO21089.5 GI:13786358
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                              80.0%; Score 16.8; DB 2; 90.0%; Pred. No. 8.1e+02; tive 0; Mismatches 2;
                                                                                                          1. .08941
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="cH230-224B2"
                                                                                                                                                                                       23763 a 19418 c 16127 g 25100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Project Name: 729006
Center clone name: CITB-H1_2264D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 100912)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                             Project Information
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Best Local Similarity
Matches 18; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
            86142
86242
87700
87800
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LOCUS
                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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                                                                                           FEATURES
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SOURCE

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LITECT. SUBMILISATION

Submitted (17-OCT-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakifenias affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:g1-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Oryza sativa
Cryza sativa
Cryza sativa
Collivar:Nipponbare) DNA, clone:0J1369_G08.

SM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.

I (bases 1 to 104188)
S Sasaki,T., Watsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:0J1369_G08
L published Only in Database (2001) In press
2 (bases 1 to 104188)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa chromosome 2 clone OJ369_G08, *** SEQUENCING IN PROGRESS ***, in ordered pieces. AP004257.1 GI:16215756 HTG: HTGS_PHASE2. Oryza sativ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 100912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
21140: gap of unknown length 24617: contig of 3477 bp in length 24717: contig of 2477 bp in length 27291: contig of 2574 bp in length 27391: gap of unknown length 36976: contig of 9585 bp in length 47599: contig of 10523 bp in length 47699: gap of unknown length 68271: contig of 20572 bp in length 68271: gap of unknown length 68371: gap of unknown length 80965: contig of 12594 bp in length 8165: gap of unknown length 87307: contig of 6442 bp in length 87307: contig of 10294 bp in length 87307: contig of 10294 bp in length 97801: gap of unknown length 97801: contig of 10294 bp in length 97801: contig of 10294 bp in length 97801: contig of 10294 bp in length 97801: contig of 3111 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CTD-2264D9"
/clone_lib="CalTech human BAC library D"
27774 a 20918 c 22009 g 29159 t 1052 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 2; Length 1
Pred. No. 8.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .100912
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 84084 TCTCGGGCTGTGGAAATAIC 84065
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, L.E., Jacobson, B., Jaive, Johnson, R., Jaivet, S., Hume, J., Jackson, L.E., Jacobson, B., Jaivet, Jacobson, B., Loure, R., Karlson, E., Karlsson, E., Karlson, E., Karlson, E., Karlson, E., Lintargeo, Lieu, C., Liu, J., Liu, W., Louser, M., Louser, B., Landry, N., Leal, B., Lewis, L. C., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., McLeod, M., Martinez, E., Massey, E., McLeod, M., Marsey, E., McLeod, M., Massey, E., McLeod, M., Massey, E., Marched, T., Moyapan, N., Mayen, M., Nayen, M., Nayen, R., Nayen, N., Nayen, N., Nayen, N., Nayen, N., Nayen, R., Nayen, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rodengren, E., Sodergen, E., Sodergen, E., Soatk, Tabor, P., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, S., Usnan, R., Warling, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Warlston, B., Weinstock, G. and Gibbs, R., Pannission

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "working draft' sequence. It currently

* consists of 67 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine Center Baylor College of Medicine Center Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 0x in Q20 bases; agarose-\hat{f}p estimation Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 135596 bases at least 040
Consensus quality: 143040 bases at least 030
Consensus quality: 148817 bases at least 020
Estimated insert size: 136955; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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9183: gap of unknown le
18088: contig of 8805 bp
18088: gap of unknown le
22682: contig of 4594 bp
22782: gap of unknown le
2786: contig of 5204 bp
28086: gap of unknown le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 3410 b
gap of unknown l
contig of 4980 b
gap of unknown l
contig of 4900 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-119J12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 172300)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36676:
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22683
22783
27987
26087
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31597
36577
36677
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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S Alabaes 1 to 172300)

S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alabrooks, S.L., Amaretunge, H.C., Are, J.R., Banks, T., Barbarta, J.,

Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouck, J., C.,

Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Coyle, M.D., Dathorne, S.R., David, R., Davis, C.,

Davy-Carroll, L., Dederich, D.A., Delaney, R.R., Delgado, O.,

Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,

Elhaj, C., Escottch, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J.,

Foster, P., Frantz, P., Gabisi, A., Ganarathe, P., Hale, S.,

Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC105570 172300 bp DNA linear HTG 12-JAN-2002
Rattus norvegicus clone CH230-119312, *** SEQUENCING IN PROGRESS
***, 67 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. .104188

//organism-"Oryza sativa"

//ob_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS AL139235 Accession AL139235
                                                                                                                                                                                                                                                                                                                                                                             Length 104188;
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                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 2;
Pred. No. 8.1e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.8; DB 2;
Pred. No. 8.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                       /clone="0J1369_G08"
30752 a 21170 c 21376 g 30890 t
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210000
310000
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90.0%; Pred
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%;
90.0%;
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Waterston, R.
Direct Submission
Submitted (28-MAR-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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Waterston, M. H.
Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, M. 05108, USA
5 (bases 1 to 194322)
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Ccenorhabditis elegans cosmid Y47G6A, complete sequence.
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 194322)
The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
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Minx, P., Graves, T. and Hawrysko, C.
The sequence of C. elegans cosmid Y47G6A
Unpublished
3 (bases 1 to 194322)
Waterston, R.
Direct Submission
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2101. 2995,3046. 3347,3399. 3521,3571. 3796,4529. 4928,
4986. 5145,5196. 5939))
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Location/Qualifiers
1. .194322
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="I"
/clone="Y47G6A"
complement(706.599)
/gene="Y47G6A.12"
/note="gene"
/note="gene"
                                                                              Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
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Submitted (16-NOV-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
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                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-07T-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, NO 63110, USA
                                                                                                                                                                                                            Submitted (30-AUG-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall cambridge CB10 IRO, England
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                                                                           Submitted (06-APR-2001)
University, 4444 Forest
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AUTHORS
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                                                                                                                                                                                                                                                                                                                           /translation="MTNSDKSTSSSASKVMRPCHIIDKWRIKALLGKGACGVVYKVED
KNRKGYCAAMKVEYDSEEFDRTLQLEVNVLSKLTDSRDVLKLIDYGKRKLYRYMVTTL
CGKDLMALRWKIQRGFNDATAMRVAVFTLYGLKQLHEAGYVHRDVKPGNIMTAANKGR
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VAMYISTYVILMGLIPWSKINSMKKSTROLALEDDPDELKS TEYLEYLLSY
AURRWYEKTY NILLMATIRIKINFLDPYEWEDDEMERWARAREKEREKEKEKEKE
KENELSADSMKTAIPAKSAKAESEVAGEVDEOKKVKDNSSGEOOODTLNVDKGNKLIS
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CNAISLLMGCGSVRTIPQALGFDGKTAILDYAWAKCPLIVGCLWTVTDGEIDRFLIRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDDCFEDSKSLTGIDKLRQLSEAMHEARSKARLKYLTGAAVVMYGLPVVAKQTTPFVE
KDQRNLPQTPKTSARTSMRMETVPKTPKQEFVTSKSVPMTPIFSNNENKSPSRARMPS
RVLKTPRQVKTFQEEDDEAPKRSTTRQLKPLVAPPIPATPTTRTRSSARTPSRSRNL
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Ekkkhiqrmqarlegsealtsdtesneaarrsreparnivegfqkvkeryrfniehie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"Hypothetical protein Y47G6A.12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CWERLPIFDEYPYVGRQVSIHSTFSQLEAMKSQEKQIPLQIDVQNAYYILDPDNNLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIAEFGVNGPIDMNSLSKLARITSYYASSEYFQGLAKYQRTACKMFITWQTLRKEAME
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12648. .13282,14331. .14479,14814. .15110)

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yk47e3.3, yk127h4.3, yk127h4.5, yk134d2.3, yk134d2.5, yk20c9.5, yk277d4.3, yk277d4.5, yk277d4.5, yk277d4.5, yk27fe1.5, yk349c7.5, yk360b5.3, yk360b5.5, yk376d8.3, yk416d8.3, yk416d8.5, yk416d8.5, yk416d8.5, yk416d8.5, yk578b6.3, yk578b6.3, yk578b6.3, yk578b6.3, yk578b6.3, yk578b6.5, yk578b6.5, yk598d10.3, yk578b6.5, yk598d10.5*
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Dipublished

E Unpublished

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Kiley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

All repeats were identified using RepeatMasker:

Smit, A. F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatWasker.html

Center: Whitched Latture in the Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACU15769 57013 bp DNA linear HTG 25-OCT-2000 HOme sapiens clone RP11-2D9, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 57013) Bliran, B. Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, Clone RP11-2D9 Uppublished
                                                                                                                                                                                                    Gaps
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                         Length 319857;
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L1509
42 others
                                                                                                                                                                                                    Indels
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                                                                                                                            Score 16.8; DB 2;
Pred. No. 7.6e+02;
0; Mismatches 2;
   56807 c 58334 g 102590
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                                                                                                                                                                                                                                                                                                                                           Db 269811 ATGTCGGGCGCTGGAACTAT 269792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC015769.3 GI:10998966
HTG; HTGS_PHASE0.
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                                                                                                                                    80.0%;
90.0%;
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                                                                                                                                                                                                                                                                               1 atgtcgggcggtggaaatat
                                                                                                                                           Query Match
Best Local Similarity 90.03
Matches 18; Conservative
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          102084 a
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       BASE COUNT
ORIGIN
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REFERENCE
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LOCUS
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TON AC06782.

N AC06782.

HTG. HTG. PHASE1.

Caenorhabditis elegans.

IISM Caenorhabditis elegans.

IISM Caenorhabditis elegans.

Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

The search.R.H.
                                                                                                                                                         join(16733. .16868,17929. .18209,19439. .20203,22406. .23211,
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                 AKDMASSRSEVNENSQYGTPAKAGNSVTGDSIDMETAIECDQMEYNSKKALPRDELQF
                                                                                                                                                                                                                                                                           /note="contains similarity to Pfam family PF00488 (DNA mismatch repair proteins, muts family), score=296.7, muss amily), score=296.7, sez_19e.85, N=1; coded for by the following C. elegans cDNAs: yklbl1.3, yklbl1.5, yk8910.3, yk8910.5, yk4704.3, yk4704.5, yk151b12.3, yk17096.5, yk78088.5, yk29088.5, yk515b12.3, yk321b5.5, yk563a9.5, yk788e06.5, yk786639.3, yk563a9.5, yk563a9.5, yk563a9.5, yk563a0.5, yk56
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Direct Submission

Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Loui Mn 63108, USA

Mn 63108, USA

On Mar 1, 1999 this sequence version replaced gi:4263156.

* NOTE: This is a "working draft" sequence. It currently consists of 4 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.8; DB 3; Length 194322;
Pred. No. 7.8e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 3652; contig of 3652 bp in length 1653 3666; gap of unknown length 1667 36798; contig of 33132 bp in length 1799 36812; gap of unknown length 1791 156243; gap of unknown length 1731 156244; gap of unknown length 1756245; contig of 119418 bp in length 1756345 319857; contig of 163613 bp in length.
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Unpublished
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16733. .29478
                                                                                         16733. .29478
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Waterston, R.H.
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90.0%;
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Best Local Similarity 90.03
Matches 18; Conservative
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17326: contig of 693 bp in length
26: gap of 100 bp
18121: contig of 695 bp in length
21: gap of 100 bp
18932: contig of 711 bp in length
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19734; contig of 702 bp in length
1314; gap of 100 bp
2057; contig of 683 bp in length
117; gap of 100 bp
21314; contig of 697 bp in length
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             2, 4398; gap of 693 bp 1.

39 3036; contig of 678 bp 1n.

77 3136; gap of 73 bp 1n.

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7005: co
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Gaps 19802 40281; contig of 80 bp in length 40382 40381; gap of 100 bp 41084 41881; contig of 702 bp in length 41084 41881; contig of 702 bp in length 41084 41981; gap of 100 bp 41188 41981; gap of 100 bp 41188 41981; gap of 100 bp 411882 41981; gap of 100 bp in length 42782 4284; gap of 100 bp in length 42345; gap of 100 bp in length 42345; gap of 100 bp in length 4537 4518; gap of 100 bp in length 45037 4518; gap of 100 bp in length 45037 4518; gap of 100 bp in length 45823 45922; gap of 100 bp in length 45829 48928; contig of 692 bp in length 45829 48928; contig of 693 bp in length 45829 48928; contig of 693 bp in length 45829 48928; gap of 100 bp in length 55897; contig of 693 bp in length 55897; contig of 693 bp in length 52173 52273; gap of 100 bp 52173 52273; gap of 100 bp 52173 52373; contig of 693 bp in length 53087; gap of 100 bp 52188 53087; ga in length 97 30805: contig of 709 bp in 6 305905; gap of 100 bp 2 31594; contig of 680 bp in 100 bp 32380: contig of 686 bp in 100 bp 32380: contig of 686 bp in 100 bp 2 3170: gap of 100 bp 2 31757: contig of 680 bp in 6845: gap of 100 bp 2 31726: gap of 100 bp 3 3172 100 bp 39601: gap of 100 b 40281: contig of 680 56205 56304: gap of 100 b 56305 57013: contig of 709 Location/Qualifiers 1. 57013 Query Match 78.1%; Best Local Similarity 94.4%; Matches 17; Conservative 33971 34071 34758 34858 35546 35646 38712

ö Score 16.4; DB 2; Length 57013; Pred. No. 1.3e+03; 0; Mismatches 1; Indels 0;

us-09-235-416-3.rge

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Signature, M. Bastlen, V. Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Noguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Choepel, Y., Colangelo, M., Camarata, J., Campoplano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodges, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gide, S., Goyette, M., Graham, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Landers, T., Landers, T., Menchers, T., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihow, T., Manga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Well, D., Ollver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Roqov, P., Roman, S., Schupback, R., Stander, S., Schupback, R., Seaman, S., Schupback, P., Soughez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Zambek, L., Zimmer, A. and Zody, M.

Direct Submission

All repeats were identified using RepeatMasker: html

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                ACUSILYS 63528 bp DNA linear HTG 03-APR-2001 Homo sapiens chromosome 11 clone RP11-371C18 map 11, LOW-PASS SOCIENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63528)
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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AC091196.1 GI:13518192
HTG; HTGS_PHASEO.
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21362 21461; gap of 2100 bp 21362 21461; gap of 100 bp 22397 22366; contig of 715 bp in length 22297 22366; contig of 715 bp in length 22308 23107; gap of 100 bp 23308 2343 2342; contig of 715 bp in length 2343 2342; app of 100 bp 2343 24717; contig of 775 bp in length 24718 24717; contig of 775 bp in length 25589 2568; gap of 100 bp 24618; gap of 100 bp 25589; contig of 771 bp in length 25589 25689; gap of 100 bp 25589; contig of 771 bp in length 25600 26399; gap of 100 bp 26600 27210; contig of 711 bp in length 26500
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49 9148: gap of 100 bp
49 9860: contig of 712 bp in length
61 9960: gap of 100 bp
61 10675: contig of 715 bp in length
76 10775: gap of 100 bp
76 11495: contig of 720 bp in length
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28044: contig of 734 bp in length
28144: gap of 100 bp
28859: contig of 715 bp in length
28959: gap of 100 bp
29571: contig of 712 bp in length
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of 710 bp in length
100 bp
of 752 bp in length
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19687 19786; gap of 100 bp
19787 20530; contig of 744 bp in length
20531 20530; gap of 100 bp
20631 21361; contig of 731 bp in length
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7399: contig of 762 bp in length
7499: gap of 100 bp
8234: contig of 735 bp in length
8334: gap of 100 bp
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31354: con
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4906: con
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4081: co
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56968: contig of 763 bp in length
68: gap of 100 bp
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0; Mismatches 1;
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51179: contig of 715 bp
                                                              47: gap of 100 bp
32975: contig of 728 bp
contig of 693 bp
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Best Local Similarity 94.4
Matches 17; Conservative
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Caaller, A., Collymore, A., Callymore, A., Cooke, P., Dearellano, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McTowl, J., Najlor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollaray, R., Stupamanian, A., Talamas, J., Peterson, K., Pollaray, V., Rilley, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Nayman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lushitted (12-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910818.

All repeats were identified using RepeatMasker.html

Lefter: Whitehead Institute/ MIT Center for Genome Center. Center: Whitehead Institute/ MIT Center for Genome Center. Center: Whitehead Institute/ MIT Center for Genome Center.
ACU10774 100511 bp DNA linear HTG 13-JUL-2000
Homo sapiens clone RP11-2G12, LOW-PASS SEQUENCE SAMPLING.
AC010774
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 105 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 946: gap of 100 bp
947 1762: contig of 816 bp in length
1763 1862: gap of 100 bp
1863 2715: contig of 853 bp in length
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contig of 845 bp in length
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                                                                                                                                                                                                                            1 (bases 1 to 100511)
Burren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
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3678: contig of 863 bp 11.
78: gap of 100 hr
4598: con**
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5538: co
                                                                                           AC010774.3 GI:9119885
HTG; HTGS_PHASE0.
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6483: r
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3678: c
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Gaps

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8350 8445; 939 of 100 bp
8450 9306; contig of 857 bp in length
9407 102801; contig of 874 bp in length
10281 103801; gap of 100 bp
112381 11315; gap of 100 bp
112382 12239; gap of 100 bp
112393 1339; ocntig of 835 bp in length
112393 1339; ocntig of 835 bp in length
112394 1323; gap of 100 bp
112395 12291; gap of 100 bp
112395 12291; gap of 100 bp
112394 1323; gap of 100 bp
112394 1323; gap of 100 bp
112395 1339; gap of 100 bp
12305 1339; gap of 100 bp
123064 1339; gap of 100 bp
123064 1339; gap of 100 bp
123065 1340; contig of 867 bp in length
1230765; contig of 867 bp in length
1230765; contig of 867 bp in length
12309 1332; contig of 867 bp in length
12309 1332; contig of 867 bp in length
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134277 13239; contig of 867 bp in length
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43051 40050; app of 100 bp in length 4001 gap of 4011 gap of 100 bp in length 5012 gap of 100 bp in length 6013 gap of 100 bp in len
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Search completed: July 25, 2002, 05:38:07 Job time: 6640 sec

Human MBSP10 polyp Human cell cycle a CDNA encoding nove Human ORFX ORF1981 CDNA encoding huma CDNA encoding nove

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Human secreted pro CDNA encoding huma Colon tumour relat Colon tumour relat Salmonella typhi D Human cancer assoc

A. terreus LovE/Sc A. terreus D4B/lov Complement system Complement system

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Human ASB-3 protel Human immune syste

Drosophila melanog Drosophila melanog A human alpha-2 ma Human nervous syst

Human immune/haema A human alpha-2 ma A human alpha-2 ma

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Scoring table:

Searched:

DNA encoding novel

Drosophila melanog

DNA encoding a hum A human alpha-2 ma A human alpha-2 ma

Drosophila melanog A human alpha-2 ma DNA encoding novel

**Drosophila** melanog

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TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; eucordegenerative disease; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinesin motor protein TL-gamma gene PCR primer.
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                                                                                                                                                                                                         AAK85566
AAH74536
ABH74534
ABL20897
ABL02077
ABL02077
ABH74533
ABH74535
AAH74536
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ABA09048
ABL33263
AAA51305
AAA51295
AAA51295
AAZ19638
          AAS21290
AAF83002
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AAS56003
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12393
8035
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W09937659-A1
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                                                                July 25, 2002, 05:44:40 ; Search time 378.07 Seconds (without alignments) 95.366 Million cell updates/sec
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1. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1981.DAT:*

2. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1981.DAT:*

3. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1983.DAT:*

4. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1983.DAT:*

5. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1984.DAT:*

6. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1986.DAT:*

7. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1981.DAT:*

8. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1981.DAT:*

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9. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

11. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

12. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

13. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1995.DAT:*

14. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1995.DAT:*

15. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1995.DAT:*

16. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

17. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

18. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

20. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

21. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na1999.DAT:*

22. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na2001A.DAT:*

23. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na2001A.DAT:*

23. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na2001B.DAT:*

23. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na2001B.DAT:*

24. (SIDSI) gcgdata/geneseq/geneseqn-embl./Na2001B.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                            1736436 segs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
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AAS44925
AAA45638
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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15.2 15.8 15.8 15.8 15.8 15.8

Score

Result š

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This oligonucleotide represents one of a claimed primer pair (see also AAX87658) that can be used in the amplification of microtubule motor protein nucleic acids, especially TL-gamma DNA or RNA from a motor protein nucleic acids, especially TL-gamma DNA or RNA from a TL-gamma (see AAX0656).

TL-gamma (see AAX06618) is a novel ATP-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family microtubule motor protein that is a member of the unc-104 family cand kinesin superfamily. The invention provides TL-gamma nucleic acids, proteins and antibodies, and methods of screening for TL-gamma nucleic acids are also used to infections and diseases caused by mutated TL-gamma, or neurodegeneration. TL-gamma nucleic acids are also used to identify polymorphic variants, alleles, homologues etc. of TL-gamma, or coher motor proteins, to generate protein structural models, for recombinant production of TL-gamma, as antisense molecules, to petection of TL-gamma, as antisense molecules, to betection of TL-gamma, as antisense molecules, to betection of TL-gamma allows differentiation between hyphal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease
New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermomyces lanuginosus kinesin motor protein TL-gamma DNA.
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                                                            Claim 7; Page 60; 75pp; English
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Matches 21; Conserval
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AAX87656
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(first entry)

This is the DNA sequence of the Thermomyces lanuginosus gene

Claim 4; Page 69-70; 75pp; English

98US-0072361. 99WO-US01355

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Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                      polymorphic variants, alleles, homologues etc. of TL-gamma, or
other motor proteins, to generate protein structural models, for
recombinant production of TL-gamma, as antisense molecules, to
produce transgenic or knockout animals, and in gene therapy.
Detection of TL-gamma allows differentiation between hyphal and
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                                  The gene was isolated
coding for TL-gamma (see AAY06618), a novel ATP-dependent, plue deficiented microtubule motor protein that is a member of the unc-1104 family and kinesin superfamily. The gene was isolated from genomic DNA by PCR amplification (see also AAX87659-61). The invention provides TL-gamma nucleic acids, proteins and antibodies, and methods of screening for TL-gamma modulators potentially useful for treating hyphal fungal infections and diseases caused by mutated TL-gamma, e.g. neurodegeneration involving anterograde axonal transport, such as Alzheimer's, parklisson's or Huntington's diseases or amyotrophic lateral clerosis. TL-gamma nucleic acids are also used to identify
                                                                                                                                                                                                                                                                                                                                                             Length 2352;
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                                                                                                                                                                                                                                                                                                             Sequence 2352 BP; 626 A; 564 C; 672 G; 490 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 20; 1
100.0%; Pred. No. 0.34;
wismatches 0;
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2000US-0665363.
2000US-0693267.
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2000US-0596193.
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P-PSDB; AAU28025.
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les 21; Conserv
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Zhao QA,
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Gaps

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100.0%; Score 21; DB 20; Length 21; 100.0%; Pred. No. 0.24; ive 0; Mismatches 0; Indels

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The invention relates to novel isolated human secreted polypeptides (I) and (II) are useful for traating and polynuclectides (II). (I) and (II) are useful for traating to proper the control of the polypeptide as well as for studying medulators of the polypeptide of the proliferation of neural cells and respectation of nerve control of the proliferation of neural cells and respectation of nerve and brain tissue and is useful for the treatment of central and paralitism of the proliferation of neural cells and respectation of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, control of stages, in addition, (I) is involved in chemoteric or central and peripheral nervous system diseases, and amyotrophic lateral control of haematopolesis and is useful for treating mysloid or light disorders, platelet disorders such as thrombocytopenia or lymphoid cell disorders, platelet disorders such as thrombocytopenia or injunct of bone, cartilage tendon, lighment and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, curver, and in tissue repair, healing of burns, incisions, curver, and in tissue repair, healing of burns, incisions, curver, and in tissue repair, healing of burns, incisions, curver, and in discusor eagence. Furthermore, (I) is also useful for teperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple solerosis, contention and treatment of lung or live fibronia, and in dispets mellitus, myssthemia gravis, allerian carbolism, catabolism, catabolism, catabolism, catabolism, catabolism, catabolism, catabolism, can
Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                   Claim 1; SEQ ID No 6; 107pp; English
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Sequence 2707 BP; 617 A; 753 C; 692 G; 645 T; 0 other;

sequences of the invention.

coding

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Gaps
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  DB 22; Length 2707;
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Score 16.2; DE Pred. No. 95; 0; Mismatches
                                                            2496 ATGTGGGGTGGGGGAATATC 2476
                                              1 atgtcgggcggtggaaatatc 21
  77.18;
85.78;
Query Match 77.1
Best Local Similarity 85.7
Matches 18; Conservative
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Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antidifammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antipsoriatic; erebroprotective; antidopolic; anticonvulsant antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetee; asthma; myeloid cell deficiency; uncer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Human secreted expressed sequence tag SEQ ID NO:2213. AAA45638 standard; cDNA; 152 BP. 21-AUG-2000 (first entry) AAA45638; AAA45638/C RESULT 

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AAA AAA43426 to MAA45925 represent specifically claimed secreted expressed sequence tags (SESTS), isolated from human, mouse, chicken and rat tassue sources. The SESTS can have a range of activities depending on the tissues they were isolated from the activities include: the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; antibacterial; antifungal; antiviral; antidiabetic; antisathmatic; vulnerary; antilucer; osteopathic; neuroprotective; antisathmatic; vulnerary; antimingerial; orthoroxides to the series of the series and antidepressant. The series can be used for gene therapy and in vaccines. The SESTS are useful as probes for the correspond to the SESTS are useful as probes for the molecules which correspond to the SESTS. Protelins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (condition disorders (lasemophilia, thrombosis), inflammatory disorders (crown) series of the series of the series of the series of the series (crown) series of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Parkinson's disease; Huntington's disease; coaquiation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
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89.5%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 748; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowman MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TGTCGGTTGGTGGAAATAT 123
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                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                          McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-317938/27
                                                                                                                                                  WO200021991-A1.
                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                     15-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs K,
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TANGO 201; TANGO 223; secreted protein; transmembrane protein;

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AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of premits and mapping relating cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor positive breast cancer, oestrogen receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                           J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Open reading frame of DNA encoding a human TANGO 201 polypeptide.
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 704 BP; 217 A; 134 C; 153 G; 194 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 599-600; 1097pp; English.
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98US-0085537.
98US-0085696.
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98US-0105877
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                                                                                                                                                                                                                                                                                                                                                                                 Escobedo J,
                                                                                                                                                                                                                                                                                                                                                         Williams LT, Escorrentinhard C, Glese K, Rarendard C, Drmanac R, Cr
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                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-2001
                                                                                                                          W09958675-A2
                                                                                                                                                                                           13-MAY-1999;
                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                              21-OCT-1998;
27-OCT-1998;
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15-MAY-1998;
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Matches
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                              proliferative disorder; neoplasm; tumour; pancreatic disorder; cirrhosis; pancreatitis; thyroiditis; goiter; Graves' disease; gastric disorder; plastritis; tumour; placential disorder; placentitis; spontaneous abortion; pulmonary disorder; atelectasis; edema; Goodpasture's syndrome; muscular dystrophy; cardiovascular disorder; lischemic heart disease; congenital heart disease; cerebral edema; cerebrovascular disease; hepatic disorder; jaundice; hepatitis; leukocytic disorder; hyperplasia; leukopenia; leukocytosis; malignant lymphoma; prostate disorder; hyperplasia; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a TANGO 201 polypeptide. The specification also describes a TANGO 223 polypeptide. These polypeptides are secreted or transmembrane proteins. Human TANGO 201 and 223 nucleic acids, proteins and their modulators are useful for treating proliferative disorders e.g. neoplasms or tumours, pancreatic disorders is a disorders of the afrenal cortex, adrenal medulla, thyroid gland (e.g. thyroiditis), golter, Graves disease, gastric disorders (e.g. gastritis or tumours), placental disorders (e.g. placentitis or spontaneous abortion), pulmonary disorders (e.g. placentitis or spontaneous abortion), placental disorders (e.g. placentitis), edema, Goodpasture's syndrome, disorders of the stelectasis), edema dystrophy), cardiovascular disorders (e.g. muscular dystrophy), cardiovascular disorders (e.g. techemic heart disease and congenital heart disease), disorders of the brash of the constant of the constant disease of the constant disorders of the constant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain (e.g. cerebral edema), cerebrovascular disease and to treat injury or trauma to the brain. They are also useful for treating hepatic disorders (e.g. jaundice, hepatitis, oirrhosis or malignant tumours), renal, testicular, intestinal disorders. TANGO 223 polynucleotides are also useful for treating leukocytic disorders (e.g. leukopenias, leukocytosis and malignant lymphomas) and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule encoding secreted or transmembrane protein useful for identifying modulators and for diagnosing and treating pancreatic, cardiovascular, liver and pituitary disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.4e+02;
); Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                  /product- "TANGO 201"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 89.5
Matches 17; Conservative
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P-PSDB; AAB08640.
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                                                                                                                                                                                                                                                       Homo sapiens
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AAA62013 standard; DNA; 1652 BP

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AAA62013

02-FEB-2001

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Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation differentiation activity, immune stimulating or suppressing activity, haematopolesis activity, issue growth activity, haematopolesis activity, issue growth activity, haematopolesis activity, anti-inflammatory activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                      Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; blophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haematopitic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and membrane
                                                                                                                                                                                                                     Hydrophobic domain protein cDNA HP03091 isolated from Liver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins comprising hydrophobic regions, such as secretory and me proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1449 BP; 458 A; 292 C; 333 G; 366 T; 0 other;
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AAA62003 standard; DNA; 1449
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99JP-0069811.
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99JP-0138169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; ss
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(PROT-) PROTEGI
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19-MAY-1999;
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16-MAR-1999)
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                                                                        AAA62003;
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                                                                        NAMES OF COLOR OF STREET STREE
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Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of ceals. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopolesis activity, tissue growth activity, and thrombolytic activity, encoded coll the protein and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                      Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; blophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                                                   Hydrophobic domain protein cDNA HP03091 isolated from Liver cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1652 BP; 526 A; 323 C; 379 G; 424 T; 0 other;
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89.5%; Pred. No. 1.5e+02;
11ve 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0326255.
98JP-0364315.
99JP-0069811.
99JP-0119299.
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(PROT-) PROTEGENE
                                                                                                                                                                                                                      gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas. The primers allow obtaining of the full-length cDNas easily without any specialised methods. AAH03166 to AAH18628 and AAH18633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito K,
, Otsuki 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1793 BP; 536 A; 372 C; 430 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 12713; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:12713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                               AAH14868 standard; cDNA; 1793 BP
                                                        29-JUL-1999; 99JP-0248036.
27-AuG-1999; 99JP-0300253.
11-ANA-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                  2 tgtcgggcggtggaaatat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2
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                                                                                                                                                                                                                                                                                                                                      AAH14868;
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Score 15.8; DB 22; Length 1793; Pred. No. 1.5e+02;

75.2%;

Query Match Best Local Similarity

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rango 201; TANGO 223; secreted protein; transmembrane protein; proliferative disorder; neoplasm; tumour; pancreatic disorder; cirrhosis; pancreatitis; tyroiditis; goiter; Graves' disease; gastric disorder; placentitis; spontaneous abortion; pulmonary disorder; placentitis; spontaneous abortion; pulmonary disorder; atelectasis; edema; Goodpasture's syndrome; muscular dystrophy; cardiovascular disorder; isohemic heart disease; confenital heart disease; cerebral edema; cerebrovascular disease; hepatic disorder; jaundice; hepatitis; leukocytic disorder; hyperplasia; leukopenia; leukocytosis; malignant lymphoma; prostate disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a TANGO 201 polypeptide. The specification also describes a TANGO 223 polypeptide. These polypeptides are secreted or transmembrane proteins. Human TANGO 201 and 223 nucleic acids, proteins and their modulators are useful for treating proliferative disorders e.g. neoplasms or tumours, pancreatic disorders (e.g. pancreatitis), disorders of the adrenal cortex, adrenal medulla, thyroid gland (e.g. thyroiditis), goiter, Graves' disease, gastric disorders (e.g. gastritis or tumours), placental disorders (e.g. placentitis or spontaneous abortion), pulmonary disorders (e.g. muscular dystrophy), cardiovascular disorders (e.g. ischemic heart disease and congenital heart disease), disorders of the brain (e.g. cerebral edema), cerebrovascular disease and to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid molecule encoding secreted or transmembrane prouseful for identifying modulators and for diagnosing and treating pancreatic, cardiovascular, liver and pituitary disorders
                                                                                                                                                                                                                            DNA encoding a human TANGO 201 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "TANGO 201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                        BP.
                                                                                                                      AAA64406 standard; cDNA; 2252
              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000WO-US04784.
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/product=
179..277
/*tag= b
78..1390
                                                                                                                                                                                           02-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179..1390
 2 tgtcgggcggtggaaatat
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P-PSDB; AAB08640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                           AAA64406;
                                                                                       RESULT 10
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WO200127277-A2
 Gerritsen ME,
Smith V, Stev
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                                                                                                                                                                                                                                                                Human secretory and transmembrane; PRO; mammalian; cancer; lung;
breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
adipocyte; A-peptide; factor VIIA; gene therapy; ss.
injury or trauma to the brain. They are also useful for treating hepatic disorders (e.g. jaundice, hepatitis, cirrhosis or malignant tumours), renal, testicular, intestinal disorders. TANGO 223 polynucleotides are also useful for treating leukocytic disorders (e.g. leukocytosis and malignant lymphomas) and prostate disorders (e.g. inflammatory diseases, hyperplasia or tumours).
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers L, Filvaroff E,
                                                                                        Score 15.8; DB 21; Length 2252;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels 0;
                                                               Sequence 2252 BP; 681 A; 444 C; 496 G; 631 T; 0 other;
                                                                                                                                                                                                                                                Human cDNA sequence encoding for PRO4321 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deforge L,
                                                                                                                                                                                          AAS21290 standard; cDNA; 2285 BP
                                                                                                                                      75.2%;
89.5%;
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2000WO-US04342.
2000WO-US04414.
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99WO-US28634.
99WO-US28551.
99WO-US28565.
99WO-US28565.
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99WO-US30911.
99WO-US30999.
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2000WO-US00277
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2000WO-US03565
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17-MAY-2000; 2000WO-US13705
                                                                                                                             2 tgtcgggcggtggaaatat 20
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                                                                                                                                                                                                                             24-OCT-2001 (first entry)
                                                                                         Query Match 75.2
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beresini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                               WO200140466-A2.
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18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
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01-MAR-2000;
20-MAR-2000;
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30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                              Homo sapiens.
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16-DEC-1999;
20-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000;
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                                                                                                                                                                                                            AAS21290;
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                                                                                                                                                                                  AAS21290
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of T-lymphocytes, the proliferation of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBSPX; cancer; preclampsia; immune system; neurological; cytostatic; gynecological; antiinflammatory; neuroprotective; inotropic; relaxant; cardiant; dermatological; gene therapy; human; MBSP10; ss.
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                                                                                                                                                                                                                                                Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS21244-AAS21518 encode for novel human secretory and transmembrane
        Gurney AL, Sherwood S;
e CK, Wood WI, Zhang Z;
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transgenic or knock out animals and can be used in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.2%; Score 15.8; DB 22;
89.5%; Pred. No. 1.5e+02;
tive 0; Mismatches 2;
A, Godowski PJ, Gurne
Tumas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
147..1597
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/product= "MBSP10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 93; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1046 tgtcggttggtggaaatat 1064
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    Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 89.5
Matches 17; Conservative
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                                              Stewart TA,
                                                                                                                          WPI; 2001-403281/43.
                                                                                                                                                                P-PSDB; AAU12218
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13-SEP-2001.
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          Hillman JL,
                    Azimzai Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                          polynucleotides encoding the MSDFX polypeptides. The MBSPX polypeptide, nucleic acid and an MBSPX antibody are useful for treating or preventing a pathology associated with the protein especially in humans. The MBSPX nucleic acid can be used to express MBSPX protein (e.g. via a recombinant expression vector in a host cell in gene therapy applications), an to detect MBSPX mRNR in a biological sample or a genetic leasion in a MBSPX gene. Disorders associated with insufficient or excessive production of MBSPX protein include cancer, preclampsia, immune system disorders and inflammation, neurological disorders, cardiovascular disorders and and muscle abnormalities. The anti-MBSPX antibodies can be used to detect and isolate MBSPX proteins and modulate MBSPX activity. The present sequence represents the nucleotide sequence of MBSP10.
                                                                                                                         Novel human polynucleotide sequences and the membrane bound or secreted polypeptides encoded by these sequences, designated \mathtt{MBSPX} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cell cycle and proliferation protein CCYPR-19 cDNA, SEQ ID NO:73.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle and proliferation protein; CCYPR; human; agonist; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia; epilepsy; arteriosclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                           Length 2437;
                                                                                                                                                                                   termed MBSPX
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 2437 BP; 739 A; 473 C; 530 G; 695 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 22;
Pred. No. 1.5e+02;
); Mismatches 2;
                                                                                                                                                                                    The invention relates to novel polypeptides,
                                                                    Boldog FL;
                                                                                                                                                              Claim 9; Page 44-47; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF59608 standard; cDNA; 2449 BP.
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99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                                                                                                                                               75.2%;
89.5%;
  99US-0159231.
2000US-0175670.
2000US-0159231.
                                                                     Shimkets RA, Lichenstein H,
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.59
                                              (CURA-) CURAGEN CORP.
                                                                                           WPI; 2001-282030/29.
P-PSDB; AAB62406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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10-NOV-1999;
             12-JAN-2000;
12-OCT-2000;
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    13-OCT-1999;
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CCYPR and agonists of CCYPR are used to treat diseases or conditions cell cycle and proliferation proteins (CCYPR), AAB60453-AAB60566.
CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR and agonists are used to treat diseases or conditions associated with coveragnession of functional CCYPR. Monoclonal or polyclonal antibodies or cCCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioinmunoasays to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonuclectides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR incledides and an be used to generate transgenic animal models of human disease, and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR.

Sissassa which can be disquosed, treated and prevented using CCYPR incolomental and cell signalling disorders, and cell proliferative disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allegies, cinclude anaemia, epilepsy, arteriosclerosis, asthma, cancer, allegies, controlled subseties mellitus, disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemia reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; sclib; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.
                                                                                                                                                                                                                                                          used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                       Human cell cycle and proliferation proteins and polynucleotides
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Bandman O;
C, Shah P;
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   Au-Young J,
2, Patterson
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89.5%; Pred. No. 1.5e+02;
tive 0; Mismatches 2;
Yue H, Au<sup>.</sup>
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                          Example V; Page 179-180; 205pp; English.
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   Tang YT,
Lu DAM,
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           Lal P,
Yang J,
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                                                                                                                   WPI; 2001-112727/12
                                                                                                                                                              P-PSDB; AAB60471.
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us-09-235-416-3.rng

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The invention relates to novel isolated numan secreted polypeptices (i) and (il) and (il) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions and injury, shock, sepsis, immune responses, and is involved in increasing heamatopoiesis, stem cell survival, bone growth and remodeling. (i), (ii) ammatopoiesis, stem cell survival, bone growth creating transgenic animals useful for studying modulators of the polypeptides well as for studying modulators of the polypeptides. (C i) induces the proliferation of neural cells and responseation of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, and brain tissue and is useful for the treatment of central and selected in addition, (I) is involved in chemotactic or chemokinetic sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopolesis and is useful for treating myeloid or lymphold cell disorders platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, clost treating osteoporoxis, osteoarthritis, bone degeneration or egeneration and treatment of lung or liver fibrosis, corpertialon injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or feugral infections, autoimmune disorders e.g. multiple sclerosis, creations and conditions, such as asthma or other respiratory problems. C returnity, matchin, carbohism, astermed or elliphing in protein, carbohism, astermed or elliphing or elliphing and elliphing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to novel isolated human secreted polypeptides (I)
                                                                                                                                                                                                                                                                                                            Ma Y, Zhou P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                                                                                                                                                                            Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                         Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 122; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequences of the invention.
                                                                   2000US-0519705.
2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0693267.
                                                                                                                                                                                                                                                                                                            Liu C, Asundi V,
Yang Y, Drmanac R
                        05-MAR-2001; 2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-589934/66.
                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU28141.
                                                                                                                                                                                                        20-OCT-2000;
                                                                                                    19-MAY-2000;
                                                                                                                            .7-JUN-2000;
                                                                                                                                                                                                                                                                                                               rang YT,
                                                                                                                                                                                                                                                                                                                                       Shao QA,
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Sequence 2495 BP; 759 A; 484 C; 553 G; 699 T; 0 other;

75.2%; Score 15.8; DB 22; Length 2495; 89.5%; Pred. No. 1.5e+02; Live 0; Mismatches 2; Indels 0; 2 tgtcgggcggtggaaatat 20 17; Conservative Best Local Similarity Matches ð

Query Match

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Gaps

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AAC76426 standard; cDNA; 2505 BP. 12 AAC76426 ID AACT

08-FEB-2001 (first entry)

Human ORFX ORF1981 polynucleotide sequence SEQ ID NO:3961.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antianaemic; gene therapy; cancer; proliferative antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; burne damage; cartilage damage; antiinflammatory disease; coaquiation; thrombosis; contraceptive; ss.

WO200058473-A2.

05-OCT-2000

31-MAR-2000; 2000WO-US08621.

31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57. P-PSDB; AAB42217 Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 3123-3124; 5507pp; English.

antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroldism, cholesterol ester storage, systemic lupus AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; noctropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive. 

Sequence 2505 BP; 774 A; 482 C; 547 G; 700 T; 2 other;

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Perfect score:

Sequence:

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Scoring table:

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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All pyrimidines are 2'-F modified
US-08-714-918-39
US-09-265-315-39
US-09-265-315-39
US-09-266-417-39
US-09-266-417-102
US-09-266-417-102
US-09-266-417-102
US-09-187-331-3
US-09-187-331-3
US-09-187-331-3
US-08-171-389-267
US-08-171-389-267
US-08-475-2288-267
US-08-475-2288-267
US-08-482-080A-267
US-08-482-080A-267
US-08-976-259-36
                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Swanson & Bratschun, L.L.C.
8400 E. Prentice Place #200
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CLASSIECATION: 435
PRIOR APPLICATION DATA:
PREDICATION NUMBER: PCT/US97/01739
FILING DATE: 30 Jan 1997
PRIOR APPLICATION NUMBER: 08/595,335
FILING DATE: 1 FEB 1996
ATTORNEY AGENT INFORMATION:
NAME: BAILY J. SWANSON, ESQ.
REGISTRATION NUMBER: 33,115
REFERENCE/DOCKET NUMBER: 33,115
REFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,228B
FILING DATE: 12-FEBRUARY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                           US-09-023-228B-91/c
; Sequence 91, Application US/09023228B
; Patent No. 6140490
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BIESECKER, GREGORY APPLICANT: GOLD, LARRY
 TYPE: nucleic acid
STRANDEDNESS: single
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US-09-023-228B-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colorado
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 STREET: 8400 E
CITY: Denver
STATE: Colorad
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14, Appl
14, Appl
14, Appl
54, Appl
54, Appl
54, Appl
55, Appl
56, Appl
56, Appl
56, Appl
56, Appl
57, Appl
                                                                                                       July 25, 2002, 05:38:29; Search time 90.93 Seconds (without alignments) 56.728 Million cell updates/sec
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Patent No. 5512
Sequence 118,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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-09-060-756-666
-08-821-119-16
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                                                                                                                                                                                                                                                                                            383533 segs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - nucleic search, using sw model
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NAME/KEY: unsure
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US-08-821-119-16/c
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Query Match 72.4%; Score 15.2; DB 3; Length 60; Best Local Similarity 85.0%; Pred. No. 26; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BIESECKER, GREGORY
APPLICANT: BIESECKER, GREGORY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
TITLE OF INVENTION: COMPLEMENT SYSTEM PROTEINS
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place #200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: OSCIPLED COUNTRY: US
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDER-FOCK 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,28B
FILING DATE: 12-FEBRUARY-1998
CLASSIFICATION NUMBER: PCT/US97/01739
FILING DATE: 30 JAN 1997
PRIOR APPLICATION NUMBER: PCT/US97/01739
FILING DATE: 30 JAN 1997
APPLICATION NUMBER: 08/595,335
FILING DATE: 1 FEB 1996
ATTORNEY-AGENT INFORMATION:
NAMM: BALTY J. SWARDSON, ESG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: NEX50/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEPRAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 666, Application US/09060756 Patent No. 6183957 GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 131, Application US/09023228B Patent No. 6140490
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                                                                                    2 tgtcgggcggtggaaatatc 21
                                                                                                           46 TGACGAGGGGTGGAAAGATC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.09
"...hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                         RESULT 2
US-09-023-228B-131/c
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APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Gordon, Stephen
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: HE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE REFERENCE: 3455-016
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 666
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ICCATION: (various positions within the sequence); ICCATION: (various positions are uncertain of bases designated as "n" US-09-060-756-666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. 582104

GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Rasmussen, Grethe
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Pest Local Similarity 85.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FLING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4107.204-US
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT TREORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REPRENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 tcttgggccgtggaaatatc 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 tgtcgggcggtggaaatatc 21
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SEQUENCE CHARACTERISTICS:
LENGTH: 2424 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10174
COMPUTER READABLE FORM:
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                                                           DB 1; Length 2424;
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Typfer, R., Bautor, J., Bothmann, H., Filsak, E.,
APPLICANT: Typfer, R., Bautor, J., Rlein, B., Martini, N.,
APPLICANT: M. Iner, A., Schulte, W., Voetz, M., Walek, J.,
APPLICANT: Schell, J.
Tyfle OF INVENTION: Promoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steinberg, Raskin & Davidson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURREWA PEPLICATION DATA:
APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR-1996
PRIOR APPLICATION NUMBER: DE PGT/EP94/02950
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
FILING DATE: 04-SEP-1993
INPORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3350 Base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1140 Avenue of the Americas CTTY: New York STATE: USA TONK
STATE: New York
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
72.4%; Score 15.2; DB 3;
Best Local Similarity 85.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 3;
                                                        72.4%; Score 15.2; D
85.0%; Pred. No. 41;
tive 0; Mismatches
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                                                                                                                                                                                                                                          RESULT 5
US-08-617-860B-3/c
; Sequence 3, Application US/08617860B
; Patent No. 6133506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: genomic Lambda FIX II
CLONE: BnACCaseg10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                      2 tgtcgggcggtggaaatatc 21
|||| || || |||||| |||||
463 TGTCCGGGGTGGACATATC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atgtcgggcggtggaaatat 20
||| || || || ||||| |||||
600 ATGCGGACGCTGGTAATAT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Brassica napus
IMMEDIATE SOURCE:
                                                      Query Match 72.48
Best Local Similarity 85.08
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Startcodon LOCATION: 2611..2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-08-617-860B-3
US-08-821-119-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Sequence 32. Application US/07/21761A
Sequence 32. Application US/07/21761A
Sequence 32. Application US/07/21761A
Sequence 32. Application US/07/21761A
SEQUENCE: CONTRIBUTION Plant Fatty Acid Synthases
CONTRIBUTION PLANTS: CALGARE, 100.
STREET: 1920 CALGARES: CALGARE, 100.
STREET: 1920 CALGARES: CALGARE, 100.
STREET: 1920 Fith Street
CONTRIES RANABLE FORM:
STREET: SALCHARE FORM:
CONTRIES RANABLE FORM:
CONTRIES RANABLE FORM:
STREET: SALCHARE STREET: CALGARES: CALGARES
CONTRIES RANABLE FORM:
CONTRIES RANABLE FORM:
STREET: 1920 CALGARES
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CONTRIES RANABLE FORM:
STREET: 1920 CALGARES
CONTRIES RANABLE FORM:
CONTRIES RANABLE FORM:
STREET: 1920 CALGARES
CONTRIES RANABLE FORM:
CONTRIES RANAB
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Sequence 12, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Thompson, Gregory A
APPLICANT: Thompson, Gregory A
APPLICANT: Thompson, Blant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESSONDERCES: A
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 15; DB 1; Length 1533; 100.0%; Pred. No. 50; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
COMPUTER: Apple Macintosh 6.0.7
SOFTWARE: MicrosoftWord 4.0
SOFTWARE: MicrosoftWord 4.0
CURRENT APPLICATION DATA:
APPLICATION WUBBER: PCT/US91/01746
FILING DATE: 19910314
                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-WAR-1991
CLASSIFICATION NUMBER: 07/615,784
APPLICATION NUMBER: 07/67,373
FILING DATE: 14-WOV-1990
PRICE APPLICATION NUMBER: 07/567,373
FILING DATE: 13-WG-1990
PRICE APPLICATION NUMBER: 07/567,373
FILING DATE: 13-WG-1990
PRICE APPLICATION NUMBER: 13-WG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-WAR-1990
ATCRNEY AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 34,719
NAME: CARI J. Schwedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (916) 753-6313
TELERA: (916) 753-1510
TELEX: 350370 CGME
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA to mRNA
US-08-471-791-12
                                         16-SEPT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 gtcgggcggtggaaa 17
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1920 Fifth CITY: Davis STATE: California COUNTRY: USA ZIP: 95616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                  FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
PCT-US91-01746-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE: 45
CORRESPONDENCE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: Apple Macintosh OPERATING SYSTEM: MacIntosh 7.1 SOFTWARE: MicrosoftWord 5.1 (a) CURRENT APPLICATION DATA:
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,687
FILING DATE: FEBRHARY 1, 1993
CLASSIFICATION BARA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE: 15-AUGUST-1991
PRIOR APPLICATION DAPR:
APPLICATION NUMBER: 07/588 493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DAPR:
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: COONTO E. SCHETE
REGISTRATION NUMBER: 34,719
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPRAX: (916) 753-6313
TELEPRAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: CDNA to mRNA US-07-978-687-32
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ZIF: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.4
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 gtcgggcggtggaaa 17
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CITY: Davis
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-471-791-12
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                                                                                                                                                                                                                                                                                    Length 1533;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER FREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PAPENDY disk
COMPUTER: PAPENDIN SELOS SOFTWARE: PAPENDIN BELOW FROM THE STATE TOWN THE STATE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCES: 40
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8; DE
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                  71.4%; Score 15; DB 100.0%; Pred. No. 50; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08616368A Patent No. 5767262 GENERAL INFORMATION:
  TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
TYPE: NUCLEEC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: CDNA to mRNA PCT-US91-05801-32
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88.9%;
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 225 Frank
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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US-08-616-368A-23
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100.0%; Pred. No. 50;
tive 0; Mismatches 0; Indels
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PCT-US91-05801-32
FCT-US91-05801-32
Sequence 32, Application PC/TUS9105801
GENERAL INFORMATION:
APPLICANT: Vic. C. Knauf
APPLICANT: Gregory A. Thompson
FTILE OF INVENTION:
CORRESPONDENCES:
CORRESPONDENCES:
STREET: 1920 Fifth Street
CITY: Davis
CONTEST CA
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-UUNE-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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95616
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CUNTRY: MA
CUUNTRY: WA
CUUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,368A
FILING DATE: 15-MAR-1996
CLASSIFICATION: 514
ATYONEY/AGENT INFORMATION:
NAME: FRASET, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REPERBUCE/DOCKET UNMBER: 05433/022001
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
COUNTER 2110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER READABLE FORM:
COMPUTER: TEM COMPACTIBLE
OPERATING SYSTEM: Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR.1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 15-MAR.1996
FILING DATE: 15-MAR.1996
ATORNEY/AGENT INFORMATION:
NAME: FRASEL' Janis K, 819
REFERENCE/DOCKET NUMBER: 05433/03001
TELECHMONICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
TELECHMONICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
TELECHMONE: G17-542-5070
TELECHMONE: G17-542-5070
TELECHMONE: SEQUID NO: 23:
SEQUENCE CHARACTERESTICS:
LENGTH: 113 base pairs
TYPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
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Pred. No. 45;
0; Mismatches
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Best Local Similarity 88.5
Matches 16; Conservative
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Patent No. 625857

GENERAL INFORMATION:
APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSED: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                               APPLICANT: Lee, Mu-En
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
APPLICANT: Yet, Shaw Feng
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: DISRUCLE
COMPUTER: IBM Compatible
COMPUTER: BEATEM Windows 95
SOFTWARE: FASTESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beatie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELECOMMUNICATION NUMBER: 05433/022002
TELEPHONE: 617/542-8906
TELEPHONE: 617/542-8906
TELEPRA: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 base pairs
TEROTH. 113 base pairs
TEROTH. 113 base pairs
TEROTH. 113 base pairs
TEROTH. 113 base pairs
TEROTH.
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88.9%; Pred. No. 45
                                                                 Sequence 23, Application US/09054298 Patent No. 6136953 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.59
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA
US-09-054-298-23
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US-08-818-655-23
                                                     US-09-054-298-23
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Gaps

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Pred. No. 58;
0; Mismatches 2; Indels
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88.9%; Pred. No. 58;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09054298
Patent No. 6136953
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FRASEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-ARR-1998
FRIGHT APPLICATION NUMBER: 08/616,368
FILING DATE: 15-YAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BEALTLE, Ph. D. Ingild A.
REGISTRATION NUMBER: 05433/022002
TELECOMMUNICATION INFORMATION:
TELEFRENCE/DOCKET NUMBER: 05433/022002
TELECAMMUNICATION INFORMATION:
TELEFRAX: 617/542-8906
TELEFRAX: 617/642-8006
TELEFRAX: 61
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
WOLECULE TYPE: DNA
US-08-616-368A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.5%;
88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.99
Matches 16; Conservative
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US-09-054-298-14
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Gaps

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2 tgtcgggcggtggaaata 19

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88 TCTGGGGCGGTGGAAATA 105
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Search completed: July 25, 2002, 05:38:32 Job time: 6620 sec

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BH378138 AG-ND-124 AG150846 Pan trog1 AG15162 Pan trog1 BE258413 60117238 BE040997 OF16802 O BH026906 RFCI -24-3 BE964839 601658494 BE966691 601661381

ALG6347 Drosophil BF128479 G01810261 AZ186641 SP\_1007\_B BB108759 BB108759 BB010176 BB010176 BBS80446 BBS80446 AA322509 EST25177 BB126311 BB126311 AA380119 EST25177 BR126311 BB126311 BB1377898 CM1-TW014

BF377896 CM1-10014 W20331 zb44d02.r1 AW799635 PM2-UM005 Z44602 HSC25B031 n W53617 md56e07.r1 AIIS7155 ud17b03.r AII20786 ub70h06.r

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB s Maximum DB s

Database

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Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.p., Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Haysshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                   BB607934 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230008G20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                     ALIGNMENTS
BIB91609
BH378138
AG153162
BE258413
BE269405
BE266906
BE964839
BE964839
BE128479
AA1825846
BB100176
BB100176
BB126311
AA322546
AA322546
BB126311
BA18933
BF377898
WZ0331
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N25409
A1120786
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                                                                                                                                                                              297
304
305
316
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LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                RESULT
BB607934
                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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BM415118 OP20190 M
B166516 1603290686
BH209290 Sm1-56P1.
BH209293 Sm1-56P1.
BG362171 9552767. y
BG409025 9585609. y
AM473489 hard-sholl.x
BF082179 MRO-BN011
B1880600 fm77b03.x
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AW829820 ra44910.y
BH53258 BOGHB87TR
BG160433 df33911.y
BF627929 HVSMED000
                                                              July 25, 2002, 04:39:04; Search time 2969.55 Seconds (without alignments) 95.447 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB607934 BB607934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                             13736207 seqs, 6748477542 residues
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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BI666361
BH205870
BH209290
BH209293
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BG409025
AW473489
BF082179
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BF627929
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em_gss_hum:*
em_gss_inv:*
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length: 2000000000
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em_estin: *
em_estov: *
em_estop: *
em_estin: *
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gb_esti: *
gb_esti: *
gb_esti: *
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460 bp mRNA linear EST 10-MAY-2001 ra44gl0.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita AWB29820
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Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Heteroderidae; Meloidogyninae; Meloidogyne.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2410127F20"
/clone_llb="RIKEN full-length enriched, ES cells"
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/lab_host="SOLR"
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1. .428
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        Automated filtration-based high-throughput plasmid preparation Automated filtration-based high-throughput plasmid preparation System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 8.1e+02;
0; Mismatches 2; Indels
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Matches 18; Conservative
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BASE COUNT

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Gaps

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RESULT 2 AV213384/C LOCUS DEFINITION

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE

AUTHORS

TITLE JOURNAL

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Washu Xenopus EST project, 1999
Washugton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinea; Xenopus.

1 (bases 1 to 668)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person, Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Contact: Sandy Clifton, Ph.D.
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/db_xref="taxon:8155"
/clone="landGE:3580245"
/clone=lib="wallcome CRC prn3 head"
/tissue_type="head, stage 30"
/lab_host="bull08 (phage-resistant)"
/note="vector: pBSRN3; Site_1: Not!; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library was constructed by N. Garrett, K. Ryan and A.M. Zorn, (Wellcome/CRC Institute).
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                                                                                                                                 1. .613
/organism="Brassica oleracea"
/strain="Toll000BH3"
/db_xref="taxon:3712"
/clone="BOGHBB7"
/clone="lb="BoGH"
/clone="tollo" | Site_1: Bstx1; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: Bstx1; 2-3 kb sheared
genomic DNA inserted into pHOS1 using Bstx1 linkers"
113 c 106 g 218 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 613;
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Best Local Similarity 90.0%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 2;
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266 ATGTCGGTGATGGAAATAT 247
        Seq primer: TR
Class: sheared ends.
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/organism="Meloidogyne incognita"
/db_xref="taxon:6306"
/clone_lib="Bird-Rao Meloidogyne incognita J2"
/clone_lib="Bird-Rao Meloidogyne incognita J2"
/dev_stage="enriched for 2nd stage juveniles"
/d
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarelshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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BOGHBB7TR BOGH Brassica oleracea genomic clone BOGHB87, DNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicacea; Brassica.
1 (bases 1 to 613)
Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Onpublished (2001)
Other_GSSS: BOGHBB7TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
The library was constructed by Uma Rao and David Bird
(david_bird@ncsu.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center St.
Louis.
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                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: McCarter JP
Contact: McCarter JP
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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Fax: 301-838-0208.
Email: cdcown@tign.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 460;
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90.0%; Pred. No. 8.9e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 438.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
BH532588
BH532588.1 GI:17754954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 90.0'
Matches 18; Conservative
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EST 06-FEB-2001

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B09467 1278 bp DNA linear GSS 14-MAY-1997 F20P3-T7 IGF Arabidopsis thaliana genomic clone F20P3, DNA
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                                                   sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104
and contains a minimum of 100 bases of phred value 20 above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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90.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16.8; DB 10; 90.0%; Pred. No. 9.8e+02;
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High quality sequence stop: 702.
Location/Qualiflers
1. 1.278
/organism="Arabidopsis thaliana"
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Seq primer: T7
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Unpublished (1997)
Other_GSSS: F20P3-Sp6
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="IGF"
/sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tgtcgggcggtggaaatatc 21
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B09467.1 GI:2090587
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Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity 90.09
Matches 18; Conservative
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/clone_lib="Hordeum vulgare seedling shoot EST library
HVCDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Vector: lambdaZAP; Site_1: Seedlings were
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes: Five-day old seedlings were
incubated at 90% RH for 24 hr. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, 600000 pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids.
These steps were performed in the TJ Close laboratory at
the University of California, Riverside (Choi, Close,
Fenton). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequence has sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticae; Hordeum.
1 (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                          792 bp mRNA linear EST 22-HVSMED0006K19f Hordeum vulgare seedling shoot EST library HVCNAMD0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMED0006K19f, mRNA sequence.
BF627929.
EF627929.2 GI:13090236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library on published (2001)
On published (2001)
On Dec 19, 2000 this sequence version replaced gi:11892087.
Contact: Wing RA
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Fax: 864 656 7288
Email: rwing@clemson.edu
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                                                                                          Length 668;
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                                                                                          80.0%; Score 16.8; DB 10; 90.0%; Pred. No. 9.5e+02; iive 0; Mismatches 2;
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/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMED0006K19f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 14
High quality sequence stop: 676.
Location/Qualifiers
                                                                                                                                                                                                                            151 TGTCTGACGCTGGAAATATC 132
                                                                                                                                                                                                    2 tgtcgggcggtggaaatatc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total hq bases = 392
                                                                                                                                                   18; Conservative
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SOURCE

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Gaps

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/strain="Puerto Rico"
/db_xref="taxon:6183"
/clone="Sml-54D8"
/clone_lib="Sml"
/note="Vector: pBeloBAC11; Site_1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH205870 161 bp DNA linear GSS 24-OCT-2001
Sml-54D8.TR Sml Schistosoma mansoni genomic clone Sml-54D8, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 161)
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of end sequences from Schistosoma mansoni (Puerto Rico strain) SM1 BAC library for gene discovery and map construction Unpublished (2001) Other_GSSs: SM1-54D8.TF
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMil824 row: l column: 22
High quality sequence start: 18
High quality sequence stop: 75.
Location/Qualifiers
1. 1406
/organism="Mus musculus"
/strain="FvB.N"
/db_xref="taxon:10090"
/clone="twAGE:5325093"
/clone="twAGE:5325093"
/sex="female, virgin"
/dsse="type="infiltrating ductal carcinoma"
/dev_stage="smonths"
/dab_note="DHIOB"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 78.1%; Score 16.4; DB 10; Best Local Similarity 94.4%; Pred. No. 1.7e+03; Matches 17; Conservative 0; Mismatches 1;
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1. .161
/organism="Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
BH205870
BH205870.1 GI:16381631
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Class: BAC ends.
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Globodera pallida.

Globodera pallida.

Globodera pallida.

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchina; Tylencholea; Heteroderidae; Heteroderinae; Globodera.

Tylencholea; Heteroderidae; Heteroderinae; Globodera.

Tylencholea; Heteroderidae; Heteroderinae; Globodera.

CE 1 (bases 1 to 1293)

Rixed Stage EST's from Globodera pallida, the potato cyst nematode (2001)

Contact: Opperman, C

Campus Box 7616; Raleigh, NC 27695, USA

Tel: 919.515.6699

Fax: 919.515.
                                                                                      OP20190 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
BM415118 GI:18381473
EST.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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90.0%; Pred. No. 1.1e+03;
iive 0; Mismatches 2;
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/db_xref="taxon:6183"
/db_xref="taxon:6183"
/clone_lib="Sml-5691"
/clone_lib="Sml-5691"
/clone_lib="Sml-5691"
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/clone_lip="Sml-6991"

mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 X the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."
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Sml-56pl.TF Sml Schistosoma mansoni genomic clone Sml-56pl, DNA
sequence.
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Sml BAC library for gene discovery and map construction
Unpublished (2001)
Other GSSS: Sml-56F1.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 161)
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
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Pred. No. 1.4e+03;
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85.78;
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Seq primer: M13 For
Class: BAC ends.
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Best Local Similarity 85.7
Matches 18; Conservative
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DB 12; Length 161;

Score 16.2;

Query Match

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1...161
/ Organism="Scalistosoma manson!"
/ organism="Scalistosoma manson!"
/ strain="Puerto Rico"
/ db_xref="taxon:6183"
/ clone="Sml-56p!"
/ clone="lb="Sml"
/ clone="lb="Sml"
/ clone="lb="Sml"
/ note="Vector: pBeloBAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBeloBAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
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Sml-56Pl.TR Sml Schistosoma mansoni genomic clone Sml-56Pl, DNA
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Other_GSSS: Sml-56P1.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 161)
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org
                                                                                                                                                                       146 ATGTCGGTCGGTTGAAATGTC 126
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Schistosoma mansoni
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Class: BAC ends.
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Eukaryota; Viridiplante; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funarildae; Funariaceae; Physcomitrella.

Bryopsida; Funarildae; Funariales; Funariaceae; Physcomitrella.

E 1 (bases 1 to 423)

Guatrano, R., Bashiardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

Leds, Wash U Moss EST Project

Lu npublished (1999)

Contact: Ralph Quatrano
Leeds, Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Libraries were constructed by Dr. Stavros Bashiardes as part of the Physocmitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. In St. Louis (USA) DNA sequencing Dy: Washington University Genome Sequencing Center For Information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk) Putative full length read vector to vector length is 424 Seq primer: -40RP from Gibco.
                                                                                          bG4U9U25 423 bp mRNA linear EST 13-MAR-2001 gb85f09.yl Moss EST library PPG Physcomitrella patens cDNA clone BCF20URCE_ID:PPG_COPYA-111218 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                              BG409025.1 GI:13315370
                                                                                                                                                                                                                                                                                                                                                            Physcomitrella patens.
                                                                                                                                                                                                                                                                                                                                                                                                     Physcomitrella patens
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1. 373

/organism="Physcomitrella patens"  
/db.zef="texaon:3218"  
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/tissue_type="gametophore: 30 day old tissue,  
ammonium-grown"  
/lab_bost="DH108"  
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L Unpublished (1999)

Contact: Ralph Quatrano Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Libraries were constructed by Dr. Stavros Bashiardes as part of the Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please context: Cella Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Glaco
High quality sequence stop: 338.
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                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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85.7%; Pred. No. 1.6e+03;
iive 0; Mismatches 3;
BG362171
BG362171.1 GI:13251268
                                                                                                                          Physcomitrella patens.
                                                                                                                                                               Physcomitrella
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Location/Qualifiers

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// organism="Physocomirrella patens"
// organism="Physocomirrella patens"
// organism="Physocomirrella patens"
// organism="Physocomirrella patens"
// one="Per Exposmer. D: PPG_COPyA-111218"
// clone_lib="Moss EST library PPG"
// tissue_type="gametophore: 30 day old tissue,
// ammonium-grown"
// lab_host="Publos"
// lab_host="Publos"
// lab_host="D: PMP1; Construction of the CDNA library was
performed by Dr. W. Gregg Clark using a modification of
the CDNA synthesis protocol developed in the laboratory of
Dr. Michael Lovett by Dr. Yulia Korshunova (personal
communication). First polyA + RNA was isolated from total
gametophore RNA using oligo dT magnetic beads. Following
this, first strand cDNA synthesis was performed on the
bead-bound polyA + RNA, during which an oligonucleotide
anchor sequence was incorporated onto the 5'-ends of the
cDNA. PCR amplification was then used to synthesize the
second strand, to amplify the double stranded DNA, and to
incorporate dUTP containing sequence symmetry introduced at
cloned into pAMP1 using the CloneAMP pAMP1 System (Life
Technologies, GibcosNE), for cloning amplification products
by a non-restriction site dependant process. The cloning
was directional based on sequence asymmetry introduced at
the ends during PCR amplification. The 3' cDNA ends are
proximal to the NotI site of the multiple cloning site in
pAMP1. This annealing mixture was transformed into
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Gaps

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Indels

18; Conservative

Matches

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ha75f01.x1 NCI CGAP_Gas4 Homo sapiens CDNA clone IMAGE: 2879545 3' similar to contains Alu repetitive element; contains element OFR repetitive element; mRNA sequence.
AW473489
AW473489.1 GI:7043595
EST.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dases 1 to 463)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 463
/organism="Homo sapiens"
/do_xef="taxon:9606"
/clone="INAGE:2879545"
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/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
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77.1%; Score 16.2; DB 9; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels (
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Pred. No. 1.7e+03;
0; Mismatches 3;
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        Best Local Similarity 85.7%;
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U01027 Crotalus sc
X84017 V.ammodytes
U01026 Crotalus sc
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D00344 Potato viru
AE008842 Salmonell
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-2026P8 map 1, LOW-PASS SEQUENCE
                                                                                                    AZ12227 Sequence
AZ122257 Sequence
AZ12265 Human DNA
AC012055 Homo sapi
AC12055 Homo sapi
AC127149 Sequence
AZ27149 Sequence
BC006431 Homo sapi
BC006431 Homo sapi
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U41564 Human adeno
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HSRNARAGA
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                             1797656 seqs, 10463268293 residues
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                                                         nucleic search, using sw model
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Score Result

TITLE JOURNAL COMMENT

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13972 13971: Contrig of 670 bp in length 13972 14641: contig of 670 bp in length 14642 1441: gap of 100 bp 14542 15522: gap of 100 bp 15523 16199: contig of 681 bp in length 15523 16199: contig of 677 bp in length 16300 16299: gap of 100 bp 16300 16297: contig of 674 bp in length 16300 16393: contig of 674 bp in length 16374 17754: contig of 674 bp in length 17755 17854: gap of 100 bp 17754 17754: contig of 681 bp in length 17755 17854: gap of 100 bp 17755 17854: gap of 100 bp 17755 17855 18540: gap of 100 bp 18541 18640: gap of 100 bp 18541 19393: gap of 100 bp 18541 19393: gap of 100 bp 18641 19393: gap of 100 bp 18641 19393: gap of 100 bp 18641 19394 20094: contig of 682 bp in length 20493: gap of 100 bp 22519 22519 22519 2389: contig of 675 bp in length 22419 22519 gap of 100 bp 23390 23394: contig of 675 bp in length 23492 2588: gap of 100 bp 24814 2588: gap of 100 bp 24814 2588: gap of 100 bp 24814 2588: gap of 100 bp 2588: gap of 200419 of 673 bp in length 25482 2581: gap of 100 bp 2588: gap of 200419 of 673 bp in length 25482 2581: gap of 100 bp 2588: gap of 200419 of 655 bp in length 25482 2581: gap of 100 bp 2588: gap of 200419 of 655 bp in length 25482 2581: gap of 100 bp 2588: gap of 200419 of 655 bp in length 25482 2581: gap of 200419 of 655 bp in length 2588: gap of 200419 of 655 bp in length 2588: gap of 20052 26501: contig of 682 bp in length 27815: gap of 20052 26501: gap of 20052 26501
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1681 bp in length
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35688 36379: contig of 692 bp in length
36380 36479: gap of 100 bp
36480 37121: contig of 642 bp in length
37122 37221: gap of 100 bp
37222 37915: contig of 694 bp in length
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               2 13211; gap of 100 bp 12 13871; contig of 660 bp ii 12 13871; gap of 100 bp ii 14611; contig of 670 bp ii 15422; contig of 681 bp ii 15522; gap of 100 bp
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contig of 687 bp
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38016 38720; contig of 705 bp
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41052: contig of 668 bp
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13111: contig of
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33266: cont
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30942: con
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               Grand-Plerre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Grand-Plerre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lanazares,R., Landers,T., Lehcocky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldin,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C., Peterson,K., Pierre,N.,
Pisant,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J.,
Vassillev,H., Viel,R., Vo,A., Milson,B., Wu,X., Wyman,D., Ye,W.J.,
Submitted (21-MAY-2000) Whitehead Institute/MIT Center for Genome
Sumit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This record contains 93 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
the record is updated, the accession number will
Goyette, M., Graham, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
center project name: L6854
Center clone name: 2026_P_8
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of 666 bp in length
100 bp
of 670 bp in length
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of 669 bp in length
100 bp
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666 bp in length
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of 697 bp in length
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of 657 bp in length
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of 679 bp in length
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of 678 bp in length
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of 694 bp in length
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1448: contig of 690 bp in length
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f 659 bp in length
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f 682 bp in length
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Web site: http://www-seq.wi.mit.edu
  Ginde, S.,
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1549 2245: cont
2246 2345: gap of
2346 3039: cont
3040 3139: gap of
3140 3798: cont
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4555: con
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6872: con
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9195: co
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5337: co
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6106: co
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8429: co
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759 1448: cc
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7651: r
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3799 3898: 9
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in length

in length

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Direct Submission
Submitted (13.707-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced g1:6468112. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                 18 10077; gap of 100 bp
18 10923; contig of 906 bp in length
18 10923; contig of 906 bp in length
24 11023; gap of 100 bp
18 12017; gap of 100 bp
18 12054; gap of 100 bp
55 13936; contig of 882 bp in length
18 12054; gap of 100 bp
18 12054; gap of 100 bp
19 1548; contig of 912 bp in length
19 15048; gap of 100 bp
19 15048; gap of 100 bp
19 15048; gap of 100 bp
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contig of 915 bp in length
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1796: contig of 905 bp in length
161: gap of 100 bp
18970: contig of 909 bp in length
170: gap of 100 bp
19979: contig of 909 bp in length
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contig of 903 bp in length
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contig of 911 bp in length
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9917: con*
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2919: cor
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        TITLE
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Baldwin, J., Barna, N., Beckerly, R., Boqualavkky, L., Boukhgalter, B.,
Baldwin, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fizhaugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, R., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vasalliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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Homo sapiens clone RP11-11448, LOW-PASS SEQUENCE SAMPLING.
AC013525
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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contig of 677 bp in length
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Homo sapiens, clone RP11-114H8
Unpublished
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Pred. No. 2.7e+02;
0; Mismatches 2;
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VERSION
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TITLE
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us-09-235-416-4.rge

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89 30,898; cont. 9 of 100 bp 111; cont. 19 of 923 bp in length 12 3111; gap of 100 bp 111; gap of 100 bp 113,2020; cont. 9 of 909 bp in length 21 33,2020; cont. 9 of 909 bp in length 13 3120; gap of 100 bp 100 bp 13 34,032; cont. 9 of 906 bp in length 13 34,032; cont. 9 of 906 bp in length 13 35,038; cont. 9 of 906 bp in length 13 35,038; cont. 9 of 906 bp in length 13 35,038; cont. 9 of 906 bp in length 15 35,038; cont. 9 of 906 bp in length 15 37,057; cont. 9 of 906 bp in length 15 37,057; cont. 9 of 906 bp in length 15 37,057; cont. 9 of 901 bp in length 15 37,057; cont. 9 of 901 bp in length 15 38,058; cont. 9 of 901 bp in length 15 38,058; cont. 9 of 901 bp in length 15 38,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 15 30,058; cont. 9 of 901 bp in length 
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23341 24040: gap of 100 bp 24041 24942 25041: contig of 901 bp in length 24942 25042 25965: contig of 924 bp in length 25042 25965: contig of 924 bp in length 26066 26065: gap of 100 bp 2657 27956: gap of 100 bp 27057 27966: contig of 901 bp in length 27057 27966: contig of 901 bp in length
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58109: contig of 909 bp in length
58209: gap of 100 bp
59113: contig of 904 bp in length
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Interact Submission

Submitted (109-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Feb 11, 2002 this sequence version replaced gi-15594038.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; WP: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 139563)

Frankland, J.
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Pred. No. 2.6e+02;
0; Mismatches 2;
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Best Local Similarity 90.9
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was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl be found at RR4-666F24 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC017777 148184 bp DNA linear HTG 09-DEC-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                             This sequence is the entire insert of clone RP4-666F24 The true left end of clone RP5-977F20 is at 96898 in this sequence. The true right end of clone RP11-109G4 is at 10338 in this sequence. Location/Qualifiers
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/note-"Single clone region. Sequence from reads from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submitted (09-DBC-1999) Celera Genomics, 45 West Gude Drive, Submitted (09-DBC-1999) Celera Genomics, 45 West Gude Drive, Stockhile, MD, USA
This sequence was Identified as CDM:10212057 by the submitter For more information on this record e-mail to fly@celera.com.
For more information on this record e-mail to fly@celera.com.
For more information on this record e-mail to fly@celera.com.
This sequence will be replaced.
This sequence will be replaced.

This sequence will be preserved.

Location/Qualifiers
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/db_xref="taxon:7227"
32955 c 32504 g 41863 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.8; DB 9;
Pred. No. 2.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.7%; Score 18.8; DB 2;
90.9%; Pred. No. 2.5e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                            /map="p13.1-13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 89983 ACTTCCTGCTTTGCTGTTTTCA 89962
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AC017777.1 GI:6553413
HTG; HTGS_PHASE2.
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90.9%;
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Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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DEFINITION
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AUTHORS
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AC017777
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SOURCE
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AL390120 155047 bp DNA linear HTG 21-NOV-2001 Homo sapiens chromosome 1 clone RP11-521N12, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.
                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (20-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Sep 13, 2000 this sequence version replaced gi:100861S7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Sequencing vector: plasmid: LOBN52; 100% of reads
Chemistry: Dye-terminator ET-amersham; 31% of reads
Chemistry: Dye-terminator ET-amersham; 31% of reads
Consensus quality: 140446 bases at least Q40
Consensus quality: 140838 bases at least Q20
Consensus quality: 150087 bases at least Q20
Insert size: 152747; sum-of-contigs
Insert size: 171843; 7.2% error; agarose-fp
Quality coverage: 3.12x in Q20 bases; sum-of-contigs Quality
Coverage: 2.96x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30625: gap of 100 bp 50010: contig of 19385 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18738: contig of 18738 bp in length
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18839 22388: contig of 3550 bp in length
22389 22488: gap of 100 bp
22489 24572: contig of 2084 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2389 22488: gap of 100 bp 22489 24572: contig of 2084 bp in length 24573 24572: gap of 100 bp 28175 28274: gap of 100 bp 28175 28274: gap of 100 bp 28275 30525: contig of 2251 bp in length
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52255: contig of 2145 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rap of 100 bp contig of 7445 bp in length
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73135 76041; cont
76042 76141; gap of
                                                                                                                         AL390120.9 GI:10120114
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100 bp

1 gaattcctgcttcgctgttttc 22

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us-09-235-416-4.rge

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87643 87742: GORLLY OLITION DE LIBERGE 87743 94188: CONTIGO DE 87743 94188: CONTIGO DE 6446 bp in length 94189 94288: gap of 100 bp 94289 94288: gap of 100 bp 94289 99184: CONTIGO OF 6446 bp in length 99189 99184: CONTIGO OF 100 bp 110049 111048: gap of 100 bp 113513 113612: CONTIGO OF 1100 bp 113513 113612: CONTIGO OF 1100 bp 113513 113612: GORLLY OF 100 bp 113513 113612: GORLLY OF 6983 bp in length 112897 12993: gap of 100 bp 1100 bp 113597 12997: gap of 100 bp 1100 bp 113583: GORLLY OF 6450 bp in length 135013 133190: GORLLY OF 6450 bp in length 135683: gap of 100 bp 1100 bp 135583: gap of 100 bp 1100 bp 135583: gap of 100 bp 115584 142033: GORLLY OF 6450 bp in length 142034 142133: gap of 100 bp 1100 bp 152845 1552944: GORLLY OF 6100 bp 1100 bp 152845 1552947: CONTLY OF 6103 bp in length 1552945 155047: CONTLY OF 6103 bp in length
87642: contig of 11501 bp in length
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ACU73977 177908 bp DNA linear HTG 19-JAN-2002 Homo sapiens chromosome 2 clone RP11-253H16, WORKING DRAFT SEQUENCE, 7 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177908)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA on Jan 19, 2002 this sequence version replaced g1:18042388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 155047;
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
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AC073977.5 GI:18250127
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44036 a 32390 c 31900 g 44412 t
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Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.7%;
Best Local Similarity 90.9%;
Matches 20; Conservative
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           misc_feature
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa, Arthropoda; Diptera; Brachycera;
Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.

1 (bases 1 to 195755)

Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,
Dugan Rocha, S.D., Sodergren, E.S., Hodsson, A.H., Chen, R.C.,
Ayele, M.A., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
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Hostin, D., Howland, T.J., Hume, J., Logwam, C., Jalali, M., Kovar, C.,
Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
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Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Xiang, J., Zaverl, J.S., Zhou, J., Zorrilla, S., Smith, H.O.,
Wheeler, D., Weinstock, G., Gibbs, R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No Direct Submission

Direct Submission

Direct Submission

Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Robert State and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX Manaratunge, H.C., Are., Nr., Barks, TX. Harris, TX. Barks, TX. Harris, TX. Barks, TX. Harris, TX. Barks, TX. Harris, TX. Barks, TX. B
               Institute Drosophila BAC library) complete sequence
                                     AC010009
AC010009.5 GI:16418028
                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 195755)
Worley, K.C.
                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
REFERENCE
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JOURNAL
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AUTHORS
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Drosophila melanogaster 3L BAC RPC198-23D16 (Roswell Park Cancer
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                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the places at snot known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 2; Length 177908;
Pred. No. 2.5e+02;
0; Mismatches 2; Indels 0:
Sequencing vector: M13; 32%
Sequencing vector: plasmid; 67%
Chemistry: Dye-primer ET; 32% of reads
Chemistry: Dye-terminator B49 Dye; 67% of reads
Chemistry: Dye-terminator B49 Dye; 67% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 172974 bases at least 040
Consensus quality: 175807 bases at least 030
Consensus quality: 175807 bases at least 020
Insert size: 160000; agarose-fp
Insert size: 157308; aum-of-contigs
Quality coverage: 12.66 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1146: contig of 1146 bp in length
1246: gap of unknown length
2420: contig of 1174 bp in length
2520: gap of unknown length
4176: contig of 1656 bp in length
4276: gap of unknown length
5991: contig of 1715 bp in length
6091: gap of unknown length
9107: contig of 3016 bp in length
9207: gap of unknown length
176414: contig of 167207 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630 others
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177908: contig of 1394 bp in length.
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4277. .5991
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6092. .9107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6092. .9107
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9208. .176114
/note="assembly_name:Contig34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1247. .2420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig6"
a 35157 c 34279 g 53411 t
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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176515. .177908
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Best Local Similarity 90.9%;
Matches 20; Conservative (
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Submitted (25-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
        (bases 1 to 195755)
JOURNAL
        REFERENCE
           AUTHORS
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JOURNAL

TITLE

REFERENCE

JOURNAL

TITLE

REFERENCE AUTHORS

Direct Submitssion

Submitted (29-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Chases 1 to 195755)

Rorley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Buday, C., Burkett, C., Binday, M., Bryanti, N.P., Burkatt, N.P., Burkett, C., Brown, M., Bryant, N.P., Buhay, C., Burtea, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, R., Chadhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M., Davis, C., Davyle, M.D., Dathorne, S.R., David, R., David, R., David, M., Draper, H., Dugan Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Lorder, C., Lorder, C., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, C., Chen, R., Chen, C., Chen Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovideo, R., Pacc, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Spark, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wallington, S., Walliams, G., Williams, G., Williams, G., Williams, G., Williams, G., Williams, G., Williams, G., Walliamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Glbbs, R.

Gaps 81.7%; Score 18.8; DB 3; Length 195755; 90.9%; Pred. No. 2.5e+02; 2; Indels 90.9%; Pred. No. 2.5e ive 0; Mismatches 20; Conservative Best Local Similarity Query Match Matches

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DD 37603 GAATIGCTGCTTCTCTGTTTTC 37624 1 gaatteetgettegetgtttte 22 ŏ

212739 bp DNA linear HTG 13-OCT-2001 Homo sapiens chromosome 12 clone RP11-673D15, WORKING DRAFT SEQUENCE, 2 unordered pieces. DEFINITION RESULT 8 AC018630

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens human.

ORGANISM

AC018630.33 GI:16041329 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.

AC018630

ACCESSION VERSION KEYWORDS SOURCE is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

151372: contig of 151372 bp in length 151373 151472: gap of unknown length 151473 212739: contig of 61267 bp in length.

Location/Qualifiers
1. .212739
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/db\_xref="taxon:9606"

source

FEATURES

consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is

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Manmallis Eutrerla; Filmates; Catafilli; Homilidae; Homo.

Manmallis Eutrerla; Filmates; Catafilli; Homilidae; Homo.

Munny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F. X., Allen, C.,

Alabrooks, S.L., Amatetunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Bowles, S., Briewel, Brown, E., Brown, B., Brynt, N.D., Bulwy, C.,

Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M. Cavasos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Chon, A.L., Dathorne, S.R., David, R., David, M.L., Davis, C.,

Dany-Carroll, L., Dederich, D.A., Delaney, K.N., Delgado, O.,

Denn, A.L., Duthin, K.J., Earnhart, C., Edgar, D., Edward, C.,

Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edward, C.,

Elhaj, C., Escotto, M., Falls, T., Ferraguco, D., Edward, C.C.,

Elhaj, C., Escotto, M., Falls, T., Ferraguco, D., Edward, J.,

Hamilton, K., Barris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,

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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Jackson, L.E., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, W.,

Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Hulyk, S., Hume, J.,

Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Martinger, R., Martinger, L., Marssey, E., Mawhiney, E., Matching, M., Maheshwari, M., Mayon, N., Nuyen, A., Nuyen, N., Nuyen, N., Nuyen, N., Nuyen, N., Nuyen, N., Sodergen, E., Sonake, T., Sparks, A., Tamerisa, K., Tangey, J., Tangy, H., Tangey, J., Taylor, C., Yaylor, T., Peters, D., Thomas, S., Usani, K., Wasquez, L., Petchers, N., Patron, S., Wallianson, A., Walleston, D., Welley, N., Walleston, S., Wall
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center follower name: sequencing vector: plasmid; M7789
Sequencing vector: plasmid; M7789
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 7% of reads
Chemistry: Dye-terminator Big Dye: 87% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 219183 bases at least Q40
Consensus quality: 221416 bases at least Q40
Consensus quality: 222879 bases at least Q30
Consensus quality: 222819 bases at least Q20
Estimated insert size: 215919; sum-of-contigs estimation Quality coverage: 8.8x in Q20 bases; sum-of-contigs estimation
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Direct Submission
Submitted (15-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2001 this sequence version replaced gi:14787084.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: HMCG
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Gaps

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Indels

81.7%; Score 18.8; DB 2; 90.9%; Pred. No. 2.5e+02; iive 0; Mismatches 2;

Query Match
Best Local Similarity 90.9
Matches 20; Conservative

1 gaattcctgcttcgctgttttc 22

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Length 212739;

102 others

65833 t

/chromosome="12" /clone="RP11-673D15" 40132 c 36532 g 6

70140 a

BASE COUNT

ORIGIN

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DNA linear HTG 30-JAN-2002 RP23-317N1, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae; Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@Sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:18307364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 219697 bases at least Q40
Consensus quality: 219697 bases at least Q20
Insert size: 220561; sum-of-contigs
Insert size: 21356; ll.3% error; agarose-fp
Quality coverage: 13.01x in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                  AL670227 220761 bp
Mus musculus chromosome 4 clone RF
PROGRESS ***, in unordered pieces.

    .220761
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bM317N1
Db 96992 GAATTCCTGCTTCCATGTTTC 97013
                                                                                                                                                                                                           AL670227.2 GI:18477084
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                 1 (sites)
Plumb, B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                      house mouse.
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Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshinan,N.V., Mobarry,C.,
Moris,J., Moshrefi,A., Mont,S.M., Moy,M., Murphy,B., Murphy,L.,
Nussken,D.R., Pacleb,J.M., Palazzolo,M., Pittani,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Strong,R., Sun,E., Syler,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Syler,E., Spradling,A.C.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,
Rorley,R.C., Wu,D., Yaoo,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhou,X., Zhu,S., Shith,H.O.,
Glbbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
Birect Submission
Rockville, MD, USA
Rockville, MD, USA
Rockville, MD, USA
Rockville, MJ, USA
Rockville, MJ, USA
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LPAGDLPLFWCKMFKLEDINRKHHLIRYEPIVEDSSSVHYLOHITLHECQGAHAELEE
MAREGGRPCLGARSIPPLACNAIVASWSRGSFVSISIRERNQNLPPRYPQCNSCPQT"

join (<35333. . 35500, 35594. . 35756, 35909. . >35937)
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Eukaryota; Metalongaster

Eukaryota; Metalongaster

Eukaryota; Metalongary arthropoda; Tracheata; Hexapoda; Insecta;

Perygota; Neoptera; Endopteryota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 29556)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,

George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X.,

Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,

Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelbon, C.R., Gabor

Miklos, G.L., Abril, J.F., Abardari, D., Ballew, R.M., Besson, K.Y.

Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Besson, K.Y.

Busam, D.A., Bulter, H., Cadieu, E., Center, P., Burtis, K.C.,

Busam, D.A., Bulter, H., Cadieu, E., Center, P., Burtis, K.C.,

Busam, D.A., Bulter, H., Cadieu, E., Center, A., Chandra, I.,

Cherry, J.W., Cawley, S., Dahlke, C., Daw, I.D., Dew, I.,

Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkoy, B.C.,

Dunn, P., Duriblin, K.J., Evangelista, C.C., Ferraer, S.,

Fleischmann, W., Fosler, C., Gabriellan, A. B., Gargh, N.S.,

Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J. H., Gu, Z.,

Hernandez, J.R., Houck, J., Hactis, N.L., Harvey, D., Hadman, T.J.,

Hernandez, J.R., Houck, J., Howthon, K.A., Howland, T.J.,

Hennandez, J.R., Houck, J., Klumel, B.E., Kodira, C.D., Kraft, C.,

Kennison, J.A., Ketchum, K.A., Klmmel, B.E., Kodira, C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295566 bp DNA linear INV 04-OCT-2000 Drosophila melanogaster genomic scaffold 14200013386036 section 7 AE003597 AE002647
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                                                             vector_side:right"
54793 c 52961 g 54975 t
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AE003597/c
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ORGANISM
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KEYWORDS
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CDS

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AL390862.24 GI:16116471
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polynucleotides
Patent: EP 1109790-A 2173 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LID. (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.7%; Score 18.8; DB 3; Length 295565;
llarity 90.9%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 2; Indels 0;
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Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
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AX122257
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                                                                                                                                                               TITLE
SOURCE
                                                                                                                                                                          Submitted (II-0CT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 158, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clonerquest@sanger.ac.uk
On Oct 12, 2001 this sequence version replaced gi:14787516.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SwISSPROT; TT:, TREMBL; WORMPEP; Information on the WORMPEP than of the feature fable with their source databases:
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Homo sapiens chromosome 4, clone RPI1-248N22, complete sequence.
AC012055 9 GI:8671944
HTG.
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http://www.sanger.ac.uk/fdp/Christ.com.nc.rom.ac.
ppi1-30G13 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
NECTOR: psAce3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-30G13 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-103A2 is at 110619 in this
sequence. The true right end of clone RP11-34M14 is at 2000 in this
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                               Homo sapiens
Subraryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
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Pred. No. 4e+02;
0; Mismatches 1; Indels 0;
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36195 a 21831 c 20733 g 33859 t
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                              Tracey, A.
Direct Submission
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AC012055/c
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, E., Gullymore, A., Cosale, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maldin, J., Mallor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M., Conto, T., Conto, M., Mheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M., Conto, M., C
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All repeats were identified using RepeatMasker:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 171943)
Bliren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-248N22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
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AC106895 179667 bp DNA linear HTG 24-JAN-2002
Homo sapiens chromosome 4 clone RP11-161D15, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Asses 1 to 179667)

Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AC106895.3 GI:18308813
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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7rpt_family"AT_rich"
37856 . 37791
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38007 . 48035
7rpt_family"AT_rich"
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complement(24164. .24289)
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AUTHORS
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Search completed: July 25, 2002, 05:39:24
Job time: 6717 sec
      AX127149.1 GI:14041137
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                                              Waterston, R. H.
Direct Submission
Submitted (13-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jan 24, 2002 this sequence version replaced gi:18141525.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer E1, 0% of reads
Chemistry: Dye-primer E1, 0% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178962 bases at least Q40
Consensus quality: 178962 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 179567; sum-of-contigs
Quality coverage: 9.03 in Q20 bases; sum-of-contigs
Quality coverage: 8.15 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: WUGSC
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7 65446: gap of unknown length
17 179667: contig of 114221 bp in length.
Location/Qualifiers
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Pred. No. 3.8e+02;
0; Mismatches 1;
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1. .65346
/note="assembly_name:Contig8"
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The sequence of Homo sapiens clone Unpublished
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/organ.sm="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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/organism="Corynebacterium glutamicum"
/db_xref="taxon:1718"
/note="Seq 1 to long (3.309.400) split in 11, seq 7065
1.800.001 2.149.980"
86896 a 98023 c 80939 g 84122 t
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                                                                                                             Corynebacterium.

1 (bases 1 to 349980)

Masagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynucleotides
Patent: EP 1108790-A 7065 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LID. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 18.4; DB 6; Length 349980; 95.0%; Pred. No. 3.7e+02; ive 0; Mismatches 1; Indels 0;
Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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Best Local Similarity 95.0
Matches 19; Conservative
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TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; eurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; PCR; primer; ss.
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AAC03476
AAX51619
AAX20106
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AAA62532
AAH22706
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AAX14159
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ABA16034
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AAK91425
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8761
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                                                                         July 25, 2002, 05:44:43; Search time 378.07 Seconds (without alignments) 104.449 Million cell updates/sec
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2. SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                               1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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Match
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Score 23

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Human ovarian tumo

Human ovarian PCR

Human secreted pro

EST clone HJ181

Mouse secreted exp

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Database

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Scoring table:

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Human secreted exp

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Human digestive sy
DNA encoding novel
Rat neurodap 1 gen

Enterococcus faeca

Human immune/haema H. pylori GHPO 491 Human CDNA sequenc

Human nervous syst Soybean 515002 reg

Human secreted Human secreted

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Human neurodap 1 g Enterococcus faeca

Enterococcus faeca Human immune/haema

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Claim 1; Page 1893; 2479pp; English.
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                                                                                                                                                                                    This oligonucleotide represents one of a claimed primer pair (see also AAX87657) that can be used in the amplification of microtubule motor protein nucleic acids, especially Til-gamma DNA or RNA from a hyphal fungus such as Thermomyces lanuginosus (see AAX87656).

Tr-gamma (see AAX06618) is a novel ATP-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family and kinesin superfamily. The invention provides TL-gamma nucleic acids, proteins and antibodies, and methods of screening for TL-gamma nodulators potentially useful for treating hyphal fungal infections and diseases caused by mutated TL-gamma, e.g. neurodegeneration. TL-gamma nucleic acids are also used to identify polymorphic variants, alleles, homologues etc. of TL-gamma, or cher motor proteins, to generate protein structural models, for recombinant production of TL-gamma, as antisense molecules, to produce transgenic or knockout animals, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the DNA sequence of the Thermomyces lanuginosus gene
New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 23; DB 20; Length 23; I Similarity 100.0%; Pred. No. 0.44; 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermomyces lanuginosus kinesin motor protein TL-gamma DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 69-70; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX87656 standard; DNA; 2352 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaattcctgcttcgctgttttca 23
                                                                                                                                 Claim 7; Page 60; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-hyphal fungal infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
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P-PSDB; AAY06618.
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Best Local Similarity
Matches 23; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09937659-A1.
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Gaps
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detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
coding for TL-gamma (see AAY06618), a novel ATP-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family and kinesin superfamily. The gene was isolated from genomic DNA by PCR amplification (see also AAX8765-61).

The invention provides TL-gamma nucleic acids, proteins and antibodies, and methods of screening for TL-gamma modulators potentially useful for treating hyphal fungal infections and classases caused by mutated TL-gamma, e.g. neurodegeneration involving anterograde axonal transport, such as Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral sclerosis. TL-gamma nucleic acids are also used to identify polymorphic variants, alleles, homologues etc. of TL-gamma, or cher motor proteins, to generate protein structural models, for recombinant production of TL-gamma, as antisense molecules, to produce transgenic or knockout animals, and in gene therapy. Detection of TL-gamma allows differentiation between hyphal and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labat I;
?, Reinhard
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Escobedo J, Garcia PD, Garcia V, Gises K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, POt D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2352 BP; 626 A; 564 C; 672 G; 490 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ16520 standard; cDNA; 466 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gaattcctgcttcgctgttttca 23
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98US-0075954.
98US-0080114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-hyphal fungal infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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03-APR-1998;
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24-FEB-1998;
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ1253 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ1532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer, The polynucleotides can also be used to screen for and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.

Sequence 466 BP; 185 A; 65 C; 97 G; 116 T; 3 other;

ö Length 466; Indels 20; ; DB Mismatches 41; Score 18.8; Pred. No. 434 GAATTCCTGCTTCCATGTTTTC 413 ö 1 gaatteetgettegetgttte 22 81.7%; 90.9%; 20; Conservative Best Local Similarity Matches 20; Conserv Query Match ŏ 셤

AAH67138 standard; DNA; 1305 **AAH67138** 

BP

(first entry) 26-SEP-2001 

AAH67138;

glutamicum coding sequence fragment SEQ ID NO: 2173.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.

Corynebacterium glutamicum

EP1108790-A2

20-JUN-2001.

18-DEC-2000; 2000EP-0127688

99JP-0377484. 2000JP-0159162. 2000JP-0280988 16-DEC-1999; 07-APR-2000; 03-AUG-2000; (KYOW ) KYOWA HAKKO KOGYO KK

Yokol H; Ochiai K, S, Hayashi M, Ozaki A; Mizoguchi H, Ando Senoh A, Ikeda M, Nakagawa S, Tateishi N,

WPI; 2001-376931/40. P-PSDB; AAG91919 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These rest useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium. Handle and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium acutain acutal in the exemplification of the present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\over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Claim 8; SEQ ID NO: 2173; 246pp + Sequence Listing; English.

Sequence 1305 BP; 232 A; 298 C; 389 G; 386 T; 0 other;

ö Gaps ö Length 1305; Indels 80.0%; Score 18.4; DB 22; 95.0%; Pred. No. 67; ive 0; Mismatches 1; Best\_Local Similarity 95.0 Matches 19; Conservative Query Match

2 aattoctgcttcgctgtttt 21

609 aattactgcttcgctgttt 628

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AAH68530/c RESULT

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Gaps

AAH68530 standard; DNA; 349980 BP

AAH68530;

(first entry) 26-SEP-2001

glutamicum coding sequence fragment SEQ ID NO: 7065.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.

Corynebacterium glutamicum

20-JUN-2001

18-DEC-2000; 2000EP-0127688

16-DEC-1999; 07-APR-2000;

99JP-0377484. 2000JP-0159162. 2000JP-0280988. 03-AUG-2000; 

(KYOW ) KYOWA HAKKO KOGYO KK.

Yokoi Ochia1 K, S, Hayashi M, Ozaki A; Ando S, Ikeda M, Mizoquchi Senoh A, Nakagawa S, Tateishi N,

WPI; 2001-376931/40.

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

Disclosure; SEQ ID NO: 7065; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived

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ABI99592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonds aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr GJ;
                                                                                                                                                                   Gaps
                                                                                                    Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other;
                                                                                                                                       Length 349980;
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                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi DNA for cellular proliferation protein #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                        80.0%; Score 18.4; DB 22;
95.0%; Pred. No. 1e+02;
tive 0; Mismatches 1;
                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                          Db 291447 AATTACTGCTTCGCTGTTTT 291428
                                                                                                                                                                                                                                                                                   AAS56002 standard; DNA; 705 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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                                                                                                                                                                                                                                                                                                                                    13-FEB-2002 (first entry)
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611495/70.
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                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU38143.
                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170955-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2000;
26-MAY-2000;
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22-DEC-2000;
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                                                                                                                                                                                                                                                                                                            AAS56002;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, or asospastic ischaemia) by measuring expression levels of particular genes (ABI99102 to ABI9912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving represent PCR primers for a mouse ischaemic condition related sequence. The represent PCR primers for a mouse ischaemic condition related sequence.
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 705;
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                                                                                                                                                                                                                                                                                                             Sequence 705 BP; 175 A; 180 C; 200 G; 150 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                               79.1%; Score 18.2; 1
87.0%; Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABI99592 standard; cDNA; 2408 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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Best Local Similarity
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03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; finmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy; chromosome 4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD08404-AAD08478 represent cDNAs corresponding to 24 human secreted protein genes, and AAE04100-AAE004170 represent the proteins they encode. AAE04172-AAE04197 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                    Human secreted protein-encoding gene 5 cDNA clone HLUDB47, SEQ ID NO:45.
                                                         Gaps
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                                 Score 17.8; DB 24; Length 2408;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- "Human secreted protein precursor" /note- "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Mature human secreted protein"
Sequence 2408 BP; 694 A; 501 C; 635 G; 578 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes mellitus and multiple sclerosis
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complement (1305..1619)
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                                                                                                                                                              AAD08438 standard; cDNA; 2288 BP.
                                                                                            211 attectgetteggtgtgttea 231
                                                                                 3 attoctgcttcgctgttttca 23
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03-AUG-2000; 2000US-0222904.
                                 Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000; 2000WO-US30629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                                                                                                                                                                                       AAD08438;
                                                                                                                                                    AAD08438/
                                                                                                                                          RESULT
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The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Stathogical conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, and season of the itssues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, descases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), postiasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, andiogenic disorders, endocrine disorders, and infections. The proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding preserved to modify storage properties. Annibudies specific for a preserved to modify storage properties. Annibudies specific for a preserved to modify storage properties. Annibudies specific for a preserved to the disorders and in chemotaxis, and can be used as a food additive or preserved to the modify storage properties. Annibudies specific for a preserved to the disorders and an be used as a food additive or preserved to the disorders and an beautify their cognate ligands.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA09012 standard; cDNA; 8734 BP
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Best Local Similarity 94.77
Matches 18; Conservative
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gene therapy; cancer; irvous system; CNS;

cytostatic;

immunosuppressant;

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peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3583; 10078pp; English.
                                                                                                                                                                                                                                                     26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                     19-JUL-2000, 2000US-0620312.
13-AUG-2000, 2000US-0653450.
14-SEP-2000, 2000US-0653191.
19-OCT-2000, 2000US-0693036.
29-NOV-2000, 2000US-0727344.
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Zhao QA, Zhou P,
                nootropic;
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                                                                                                                                                                              WO200153312-A1.
                                                                                                        leukaemia; ss
                                                                                                                                               Homo sapiens.
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09-JUL-2000;
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                                                                                                                                                                                                                                          Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The sequences ABA08225-ABA09574 represent nucleic acids encoding them. The Invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of detecting the nucleotides. CC or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides of the invention have homology to known proteins, thereby compounds which into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth activity; and hence contentiation activities; stem cell growth activity; haematopolesis requilatory activity; itssue growth activity; hematopolesis requilatory activity; itssue growth activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activity; activity; activity, activities, haemostatic, thrombotic or thrombotic activity, activities, haemostatic, thrombotic activity, activity, activities, haemostatic, activity, activity, activity, activities, and and activities, and anormal conditions, e.g., by protein or gene therapy. Such conditions and anormal product activity, activity, and activity, activity, and anormal activity, activity, activity, and activity, activity, and activity, activity, and activity, and anormal activity, activity, activity, and activity, activity, and activity, activity, and activity, activity, and activity,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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Pred. No. 2.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                  Claim 1; Page 696-698; 1963pp; English.
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ID AAI59594 standard; cDNA; 8734
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                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                              e.g. arthritis and cancer -
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                                                                                     WPI; 2001-457740/49.
P-PSDB; ABB11768.
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Best Local Similarity
Matches 18; Conserv
                (HYSE-) HYSEQ INC.
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Wang D;

Ren F, Warng J;

Qian XB, Yang Y,

2000US-0488725. 2000US-0552317. 2000US-0598042.

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The Invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as an encopathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CNNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
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ID AAI57808 standard; cDNA; 8761 BP.
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Best Local Similarity 94.7*
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                  DNA encoding novel human diagnostic protein #21465.
AAS85661/c
ID AAS85661 standard; cDNA; 8785 BP.
                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2000; 2000US-0649167
                                                                                             13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG21474
                                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                         11-0CT-2001
                                                         AAS85661;
                                                           The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer sy, Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, War
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8761 BP; 2551 A; 1778 C; 1784 G; 2648 T; 0 other;
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Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                       Human polynucleotide SEQ ID NO 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0598042.
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                 22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                   WO200153312-A1.
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                          leukaemia; ss
                                                                                                                                                                                                                                Homo sapiens.
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09-JUL-2000;
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Zhao QA,
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Tang YT;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in esponsible for genetic disorders or other traits to assess biodiversity and and produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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Claim 1; SEQ ID No 21465; 103pp; English.
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Gaps

75.7%; Score 17.4; DB 22; Length 8761; 94.7%; Pred. No. 2.2e+02; 1ve 0; Mismatches 1; Indels 0;

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14-SEP-2000; 2000US-0232399.

14-SEP-2000; 2000US-0232400.

14-SEP-2000; 2000US-0232401.

14-SEP-2000; 2000US-0233064.

14-SEP-2000; 2000US-0233064.

14-SEP-2000; 2000US-0233065.

21-SEP-2000; 2000US-023365.

21-SEP-2000; 2000US-0234274.

25-SEP-2000; 2000US-023498.

27-SEP-2000; 2000US-023484.

27-SEP-2000; 2000US-023634.

27-SEP-2000; 2000US-023634.

28-SEP-2000; 2000US-023636.

29-SEP-2000; 2000US-023636.

20-CT-2000; 2000US-0237039.

20-CT-2000; 2000US-0231786.

20-CT-2000; 2000US-0231808.

20-CT-2000; 2000US-0241808.

20-CT-2000; 2000US-0241808.

20-CT-2000; 2000US-0241808.

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20-CT-2000; 2000US-0241808.
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2000US-0246609.
2000US-0246610.
2000US-0246611.
2000US-0246613.
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2000US-0246526.
2000US-0246527.
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2000US-0251988
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20 - OCT - 2000;
01 - NOV - 2000;
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17-NOV-2000;
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17-NOV-2000;
     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32188
     AAK77376 standard; DNA; 4016 BP
                                                                                                                                                                                                        2000US-0179065.
2000US-0180628.
2000US-018664.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-0205515.
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2000US-0227182
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                                               (first entry)
                                                                                                                                           WO200157182-A2
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26 - JUL - 2000;
26 - JUL - 2000;
26 - JUL - 2000;
14 - AUG - 2000;
15 - AUG - 2000;
16 - AUG - 2000;
17 - AUG - 2000;
18 - AUG - 2000;
10 - SEP - 2000;
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                        Homo sapiens
                                               07-NOV-2001
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2000US-0186350
2000US-0189874
2000US-01990076
2000US-020515
2000US-020515
2000US-0205467
2000US-0215135
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2000US-0224518.
2000US-0224519.
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2000US-0217487
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2000US-0218290.
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2000US-0232080
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07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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14 - NuG-2000)
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22-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
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05-SEP-2000;
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12-SEP-2000;
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                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cc expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cs supplement the patients own production of (I). Additionally, (I)
cc supplement des may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent.

cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703
cc cancers and cancer metastases of haematopoietic antigen genomic
co AAK87694 represent invention. AAK54942 to AAK84950 and AAM82169
cc represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 32188; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.8%; Score 17.2; DB 22; Length 4016; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;
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AAK77377/c
ID AAK77377 standard; DNA; 4762 BP.
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05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251990.
                                                                                                                                                      Barash SC, Ruben
                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                               WPI; 2001-483426/52
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87950 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
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              Disclosure; SEQ ID NO 32189; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4762;
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Pred. No. 2.5e+02;
0; Mismatches 3;
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Best Local Similarity 86.4%;
Matches 19; Conservative C
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97US-0833457.
97US-0881227.
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P-PSDB; AAW98440.
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01-APR-1997;
24-JUN-1997;
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08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
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08 - NOV - 2000;
17 - NOV - 2000;
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This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these ulcer diseases, e.g. gastric and atrophic gastritis, and peptic ulcer diseases. e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used detection and diagnosis.
                     Claim 1; Page 756; 2054pp; English.
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Sequence 360 BP; 160 A; 64 C; 71 G; 65 T; 0 other;

ö Gaps ö 73.0%; Score 16.8; DB 19; Length 360; 90.0%; Pred. No. 3.1e+02; Live 0; Mismatches 2; Indels 0 Query Match 73.0° Best Local Similarity 90.0° Matches 18; Conservative

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1: /cgn2_6/ptodatca1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodatca1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodatca1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodatca1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodatca1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodatca1/ina/PCTUS_COMB.seq:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-058-260-15
US-09-058-260-17
US-08-08-260-1
US-08-08-260-1
US-08-694-078-1
US-08-694-078-1
US-08-47-4140-15
US-08-47-43-415
US-08-47-545-15
US-08-47-545-15
US-08-478-341-15
US-08-996-733-15
US-08-996-733-15
US-08-91-083-211
US-08-91-083-211
US-08-91-083-211
US-08-91-083-211
US-08-91-083-211
US-08-91-083-211
US-08-474-140-9
US-08-477-630-8
US-08-477-630-9
US-08-477-630-9
US-08-477-630-9
US-08-477-630-9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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23
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Perfect score:
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Sequence 1, Appl1
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 16, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 57, Appl
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APPLICANT: Chen, H.
APPLICANT: Chen, H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1998-10-28
EARLIER PRILICATION NUMBER: 60/106,056
EARLIER PRILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER APPLICATION NUMBER: 60/086
EARLIER PILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
NUMBER FESTEED FOR WINDOWS VERSION 3.0
      Sequence Sequence Sequence
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US-08-478-341-9

US-08-996-733-8

US-08-996-733-9

US-08-996-733-9

US-08-953-334-4

US-09-563-869A-4

US-08-155-005A-16

US-08-163-391-57

US-09-060-610-57

US-09-060-610-57

US-09-060-610-57

US-08-113-968-4-1015A-14
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82.6%; Pred. No. 87;
ive 0; Mismatches
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; Sequence 15, Application US/09058260B
; Patent No. 6218167
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-268-992-7; Sequence 7, Application US/09268992; Patent N. 6342351; GENERAL INFORMATION:
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APPLICANT: Alkens, John
APPLICANT: Fonstein, Michael
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity 85.7%;
Matches 18; Conservative
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 85.7
Matches 18; Conservative
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; LOCATION: (1182)...(2690)
US-09-058-260-1
                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (258)..(1766)
US-09-058-260-27
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US-09-058-260-1
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US-09-058-200-2/
Sequence 27, Application US/09058260B
Patent No. 6218167
GENERAL INCRMATION:
APPLICANT: Allen, Larry
APPLICANT: Alkens, John
APPLICANT: Ponstein, Wichael
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
TTILE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REPERENCE: 95-963-H
CURRENT PILING DATE: 1999-04-10
EARLIER APPLICATION NUMBER: 60/001,995
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER APPLICATION NUMBER: 60/009,704
EARLIER PILING DATE: 1996-06-12
EARLIER PILING DATE: 1996-06-12
EARLIER PILING DATE: 1996-06-12
EARLIER PILING DATE: 1996-08-07
EARLIER PILING DATE: 1996-08-07
EARLIER PILING DATE: 1996-08-08
EARLIER PILING DATE: 1997-01-10

EARLIER PILING DATE: 1997-04-11
APPLICANT: VOICE DATE OF STATE OF STATE
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; LOCATION: (196)..(1689)
US-09-058-260-15
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LENGIH: 2345
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FRESULT APPLICATION OF ARTIFICIAL Sequence FRANCES:

OTHER INFORMATION DESCRIPTION OF ARTIFICIAL SEQUENCE: Cloned esterase OTHER INFORMATION DESCRIPTION OF ARTIFICIAL SEGUENCE: CONTRICT SEGUENCE (250)..(1765)

US-09-58-206.7

DOWEY WARCH COS STAILAILY 85.74 pred: No. 81; 3; Indels 0; Gaps 0; MARCHES 181. CONSERVABLE 85.74 pred: No. 81; 3; Indels 0; Gaps 0; MARCHES 181. CONSERVABLE 85.74 pred: No. 81; 3; Indels 0; Gaps 0; MARCHES 181. CONSERVABLE 220

RESULT 4

NATIONAL APPLICATION OF ARTIFICATION OF ARTIF
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US-08-781-802-9

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OTHER INFORMATION: /note= "E001, longest open reading OTHER INFORMATION: frame; other possible start codons at ATG/met5; GTG/val8; OTHER INFORMATION: GTG/val10; TTG/leu17"
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALENS, DAIN
APPLICANT: ALKENS, DAIN
APPLICANT: PONSTEIN, Michael
APPLICANT: PONSTEIN, Michael
APPLICANT: VENTEIN, Werenika
APPLICANT: VENTEIN, Verenika
APPLICANT: CASADABAN, Malcolm
APPLICANT: ASADERS: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 310 S. Wacker Drive 32nd Floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ADDRESSE: MCDONNER STATE: 111inois
COUNTRY: USA
ADDRESSE: MCDONNER STATE: AND STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION NUMBER: US 60/019,995
FILING DATE: 11-JAN-1996
PRIOR APPLICATION NUMBER: US 60/01,995
FILING DATE: 11-JAN-1996
PRIOR APPLICATION NUMBER: US 60/01,995
FILING DATE: 11-JAN-1996
PRIOR APPLICATION NUMBER: 37,293
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-E
TELECOMMUNICATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-E
TELECOMMUNICATION NUMBER: 37,293
REFERENCE/DOCKET NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                      Sequence 1, Application US/08781802
Patent No. 5969121
3340 GAATCCCTCCATCGCTGTTTT 3360
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LENGTH: 4115, Desc. F.
TYPE: nucleic acid
STRANDEDNESS: single
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1182..2690
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APPLICANT: ALLEN, LAIRY
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LOCATION: 118:
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US-08-781-802-1
                                                                                                                                                                                                                     US-08-781-802-1
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LOCATION: 1397..2905
OTHER INFORMATION: /note= "E019 sequence of longest
OTHER INFORMATION: open reading frame; upstream untranslated region not exact"
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                                                                                                                                                         APPLICANT: ALLEN, Larry
APPLICANT: AIKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: FONSTEIN, Veronika
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADARAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 3545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION NUMBER: US/08/781,802
FILING DATE: 07-AUG-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 11-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 11-JUN-1996
PRIOR APPLICATION NUMBER: US 60/001,995
FILING DATE: US-DATA:
APPLICATION NUMBER: 37,293
REFERENCE/COMMUNICATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive 32nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 16.2; D
85.7%; Pred. No. 86;
iive 0; Mismatches
                       Sequence 9, Application US/08781802
Patent No. 5969121
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.75
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat_peptide;
; LOCATION: 1397..2905
US-08-781-802-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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DB 2; Length 4315;

70.4%; Score 16.2;

Query Match

1 gaattcctgcttcgctgtttt 21

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US-08-694-078-1

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Sequence 8, Application US/09008979A

Factoric No. 6080914

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

TITLE OF INVENTION: Strawberry Promoters and Genes

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STARE: TAXAS

COMPUTER: USA

IP: 77210-4433

COMPUTER: EDOPPY disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: DECOMPATION: PC-DOS/NS-DOS

COMPUTER: DECOMPATION PC-DOS/NS-DOS

COMPUTER: D
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                                 Gaps
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APPLICANT: Conner, Timothy W.
TITLE OF INVENTION: Strawberry Promoters and Genes
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLICASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rannerer, Particia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: 29,775
RELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,979A
                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 3;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
85.7%; Pred. No.
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                                                                                                                                                                       DD 3125 GAATCCCTCCATCGCTTTT 3145
                                                                                                                     1 gaatteetgettegetgtttt 21
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89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ttcctgcttcgctgttttc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 TTTCTGCTTCTCTGTTTC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 68.7
Best Local Similarity 89.5
Matches 17; Conservative
    Best Local Similarity 85.7
Matches 18; Conservative
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COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-008-979A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-460-618-8
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frame; other possible start codons at ATG/met5; GTG/val8;
GTG/val10; TTG/leu17"
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ALLEN, LAITY
APPLICANT: AIKENS, John
APPLICANT: AIKENS, John
APPLICANT: FONSTEIN, Michael
APPLICANT: FONSTEIN, Veronika
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Blocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 8
CORRESPONDENCES ADDRESSE: McDonnell Boehnen Hulbert & Berghoff, Ltd.
STREET: 300 S. Wacker Drive 7th Floor
                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REACHINE FORM disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIANS-DOS
SOFTWARE: PATENTIAN PATA:
APPLICATION NAMER: US/08/694,078
FILING DATE: US/08/696
FILING DATE: US/08/08/696
FILING DATE: US/08/696
FILING DATE: US/0
                                                  Mismatches
        Best Local Similarity 85.7%; Pred. No. Matches 18; Conservative 0; Mismat
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08694078 Patent No. 6218163 GENERAL INFORMATION:
                                                                                                                                 REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4315 base pairs
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1182..2690
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1182..2690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1182..269
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 300 S. W. CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
; LOCATION:
US-08-694-078-1
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Query Match

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Gaps

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PULLULANASE, MICROORGANISMS WHICH PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS PULLULANASE AND THE USES THEREOF 15
                                                                                                                                                                             Length 431;
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                                                                                                                                                                                                                     4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: nuc.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2000C
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRETING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/477,630
FILING BATE: 07-OUN-1995
FILING BATE: 07-OUN-1995
FILING BATE: 07-OUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.8%; Score 15.6; DB 1;
81.8%; Pred. No. 1.2e+02;
Live 0; Mismatches 4;
                                                                                                                                                                           Score 15.6; DB 1;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Wilhiem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
RELECOMMUNICATION NUMBER: 4121-42
TELEFHONE: (202) 429-0625
TELEFHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                      US-08-477-630-15

Sequence 15, Application US/08477630

Patent No. 5721128

GENERAL INFORMATION:
                                                                                                                                                                                                                                                         2 aattcctgcttcgctgttttca 23
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                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
US-08-474-140-15
                                                                                                                                                                         67.8%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 431 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 81.83
Matches 18; Conservative
      431 base pairs
                                                                                                                                                                       Query Match 67.8
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
PROI TITLE OF INVENTION:
NUMBER OF SECUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                      nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2000 K St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-472-293-15
      LENGTH:
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Patent No. 5721127

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: PROLUGANASE, MICROORGANISMS WHICH

TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS

TITLE OF INVENTION: PLUIDANASE AND THE USES THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.

STREET: 2000 K Street, N.W., Suite 200

STATE: D.C.

COUNTRY: Washington

STATE: D.C.

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 4; Length 752;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Rammerer, Patricia A.
REGISTRATION NUBER: 29,775
REFERENCE/DOCKET NUBBER: WOBT:058 (38-21(10613)A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 789-1438
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TENET: nucleic acid
STRANDEDNES; double
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE ZOOD

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPALIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
FILIAG DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,979
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERENCE/POCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 429-0625
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 89.5
Matches 17; Conservative
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US-09-460-618-8
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US-08-474-140-15
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Gaps

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STRANDEDNESS:
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US-08-478-341-15
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Sequence 16.
Sequence 17.
Seque
Sequence 15, Application US/08472293

Patent No. 5731174

GENERAL INFORMATION:

GENERAL INFORMATION:

FULLIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS TITLE OF INVENTION: PULJULANASE AND THE USES THEREOF NUMBER OF SEQUENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCE SITEMAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 4121-44
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: nucleic acid US-08-472-293-15
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Best Local Similarity 81.8%;
Matches 18; Conservative
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EDNESS: single
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ... STATE: D.C.
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CITY: Washington
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RESULT 15
US-08-996-733-15
Sequence 15, Application US/08996733
Patent No. 6074854
GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
MUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
STREET: --- alto.
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Ouery Match 67.8%; Score 15.6; DB 1; Length 431; Best Local Similarity 81.8%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 4; Indels
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ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,733
FILING DATE: 23-DEC-1997

PRIOR APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09301278
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09301156
FILING DATE: 15-JU1-1993
FILING DATE: 28-DEC-192
ATTORNEY/AGENT INPOMMATION:
TELEPHONE: (650) 846-7620
TELEPHONE:
                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
US-08-478-341-15
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DB 3; Length 431;

67.8%; Score 15.6;

Query Match

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                                                                                         Results file seq2-1-1071aa.res made by bobryen on Tue 23 Jul 102 15:28:45-PDT.
                                                                                                                                                                                 Results of the initial comparison of US-09-235-416-2 (1-1071) with: File : USO9235416A.pep
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278
                                                                                                                             Query sequence being compared:US-09-235-416-2 (1-1071)
Number of sequences searched:
Number of scores above cutoff:
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Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
                                                   FastDB - Fast Pairwise Comparison of Sequences Release 5.4
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168
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Threshold level of sim.
Translation Frame
Mismatch penalty
Gap penalty
Gap secore
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 Scores:
 Mean 357 0 0.00
 Median 0.00
 Standard Deviation 0.00

 Times:
 CPU 0.00
 Total Elapsed 00:00:00:00
 00:00:00:00

 Number of residues:
 784 00:00
 Number of sequences searched: 1
 1

 Number of scores above cutoff:
 1
 1

SEARCH STATISTICS

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Frame	-							
ig. Frame	. 0		200	70 WSFD   1   WSFD 70	2 - 2 K	RTVA      RTVA	LSTI	K K K 360
Sig.	0.00		0.00	RSYN 	140 RINI 1140	NKAI   I       NKAI	NRSI 	DSAI
n			111	'AFD      AFD	MFR 	210 IDEGNI           IDEGNI 210	280 GAEI        GAEI 280	RYA 
Opt. Score	357		ance as	60 PKAF           PKAF 60	0 - 0	EN L'A	LKEG LKEG	350 LSTL         LSTL 350
	357		fica	MDG!	130 130 130	0 0EII 0EII	GAR     GAR	EET.
H S ∣	1		Significance Mismatches	KTI 	HGV HHGV	200 /RSFQ1 	270 TGAT       TGAT 270	OINE
gth	84	16A		S0 RKSC HIII RKSC 50	YGKE         YGKE	KEY KEY	ATS1	340 SPAD:       SPAD: 340
Length		Application US/09235416A	Optimized Score = 357 Matches = 357 Conservative Substitutions	X 10 80 80 80 70 80 80 80 80 80 80 80 80 80 80 80 80 80	140	150 160 170 180 190 200 210  DKNLTCCTVEVSYLEIYNERVRDLLNPSTKGNLKVREHPSTGPVYEDLAKLVVRSFQEIENLADEGNKARTVA	220 230 240 250 260 270 280 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 270 280 280 280 280 280 280 280 280 280 28	90 300 310 320 X GRVIAALADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK
	as	7092	itut	PGAE 	KSYS       KSYS	190 PYVED             190	260 DLAG 	TAM1
	Application	'sn	bst	40 11PP 11PP 40	6861 	STG   - -  STG	SLV	330 NSMT/           NSMT/ 330
	cat	ion	Score ve Su		110 7607 7607 7607 110	180 VREHP       VREHP 180	/AKI      /AKI	99718 
	ppl	icat	d Sc tive	EGNC H H H EGNC	IFA)   	LKVI	250 TEK 111 250	O LKD
	<b>4</b>	\pp1	Optimized Matches Conservati	30 VRM 30	NNC	N H H	A H	320 TWLLE 1111 TWLLE 320
c	US-09-235-416-1 Sequence 1,	1, 4	Optimiz Matches Conserv	AKC]	100 FKGY1 FKGY1 100	170 LNPS1             LNPS1 170	DEE           DEE	DSVI  - -  DSVI
Description	nen			DRG DRG	DNA       DNA	DELL DELL	240 )KWHI   1   )KWHI 240	310 LVPYR         LVPYR 310
cripti	Seq	(1-1071) Sequence	357 1008 0 0	20 AREI 1   1   AREI 20	VPII	ERVE 1111 ERVE		310 NQLVP)        NQLVP) 310
Desc	6-1			PFN)	90 DLGVI 1111 DLGVI 90	160 EIYN  - -  EIYN  160	FIL.	OKKI 
	5-41	16-2 16-1	: A	7RVR     RVR	OLFO 	SYLE SYLE SYLE	230 SHAVI         SHAVI 230	300 MSSGK 
e e	-23	US-09-235-416-2 US-09-235-416-1	Score Identity ion Frame	10 7 10	80 ARQEI             ARQEI 80	VEVS 	SSRS 	30 ADMS 1       30 30
Name	60-	-23	Score Ident	GNI 	B NYA 111	150 LTCT      LTCT	INET	AAL AAL
ence	Sn .	50-s	ial due slat	MSGG MSGG MSGG	KNAF         KNAF	DKNI DKNI DKNI	220 ATNMI      ATNMI 220	290 GRV1           GRV1 290
Sequence	ד	1. 00	Initial Score Residue Identity Gaps Translation Frame					0 0
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                                                                                Results file seq2-1327-1803-aa.res made by bobryen on Tue 23 Jul 102 15:29:45-PDT.
                                                                                                                                                                    Results of the initial comparison of US-09-235-416-2 (1327-1803) with: File : US09235416A.pep
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                                                                                                                   Query sequence being compared:US-09-235-416-2 (1327-1803) Number of sequences searched: 1 Number of scores above cutoff: 1
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Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106
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                                              FastDB - Fast Pairwise Comparison of Sequences Release 5.4
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00:00:00
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168
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0.05
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159
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity matrix PAI
Threshold level of sim.
Translation Frame
Mismatch penalty
Gap penalty
Cap size penalty
Cutoff score
Randomization group
> 0 < 0 | 0 IntelliGenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCORE 0
STDEV
                                                                                                                                                                                                          100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Times:
```

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

	Score Score S
<ol> <li>US-09-235-416-1 Sequence 1, Application US 784</li> <li>US-09-235-416-2 (1327-1803)</li> <li>US-09-235-416-1 Sequence 1, Application US/09235416A</li> </ol>	784 159 159 0.00 5416A
159 Optimized Score - 159 100% Matches - 159 0 Conservative Substitutions	159 Significance 0.00 159 Mismatches 0.
X 10 20 30 40 50 QSEKLYRDENQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMP 	30 40 50 EREALLEELGISIEKGFVGPYHSKEI 
60 100 120 HLVNLSDDPLLAECLVYNIKPGGTRVGHVNQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNG 	100 120
130 140 X VRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAER  11	NSQLGSPAP 620

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```
Results file seg2-1804-2352-aa.res made by bobryen on Tue 23 Jul 102 15:30:46-PDT.
                                                                                                                                                                                                 Results of the initial comparison of US-09-235-416-2 (1804-2352) with: File : USO9235416A.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                        Query sequence being compared:US-09-235-416-2 (1804-2352) Number of sequences searched: 1 Number of scores above cutoff: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEARCH STATISTICS
                                                       FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-tuple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARAMETERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.00
0.05
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. 16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity matrix PAM Threshold level of sim. Translation Frame Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group
> 0 < 0 | 0 IntelliGenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCORE 0
                                                                                                                                                                                                                                            100-
```

Number of residues:

Number of sequences searched:

Number of scores above cutoff:

The scores below are sorted by initial score.

Significance is calculated based on initial score.

Standard Deviation 0.00

Median 0

Mean 183

Scores:

Times:

Total Elapsed 00:00:00:00

CPU 00:00:00.00 A 100% similar sequence to the query sequence was found:

аше	-					
Sig. Frame	00.00		000	SGKDS GCKDS GCKDS	TIDN	
	o		0.0	SPHFRGS	120 #SNG 	
re	83		y III	SPLI       SPLI	SDKYI SDKYI	
Scc	183 183		canc	40 DSRSI             DSRSI 640	FPV	× 5 – 5 ×
Init. Opt. Score Scor	183		Significance Mismatches	ADGD ADGD ADGD	110 SQSSF1       SQSSF1 710	180   KTAKQ               KTAKQ 780
th S	784	ę,	Sig Mis	O AGSD IIII AGSD	EDSD      EDSD	EALK      EALK
Init. Opt. Length Score Score	7	3541	183 183 ions	30 FLSKAC I I I I I I FLSKAC 630	100 LVEDN        VEDN 700	AOME 
_	us	7092;	tut	HDR.	RRGL/ RRGL/	170 2000A( 11111 2000A( 770
	ton	'Sn 1	Optimized Score = 183 Matches = 183 Conservative Substitutions	X 10 20 30 40 50 QEOSLLRHSVTNSQLGSPAPGRHDRTLSRAGSDADGDSRSDSPLPHFRGRDS 	RAVI	ZEEL!           REL!
	icat	tion	core e Su	15970 1110 1100 1000 1000 1000 1000 1000 1	90 VQKAJ           VQKAJ 690	160 ASNVDV 111111 ASNVDV
	Appl	lica	ed S ativ	TNSC           NSC	LFDI	160 ODASNV        ODASNV
	٦,	App	Optimized Score Matches Conservative Sub	10 RHSV      RHSV	80 ELDA        ELDA	KKSK       KKSK
ion	ence	352) e 1,	Opt Mat Con	OSEL       SEL	8 LTDDE       LTDDE	150 LFFGDI LFFGDI 750
ript	Sequ	34 - 2 Jenc	183 1008 0 1	X QE    RAERQE 600 X	KISH      KISH	SDAL      SDAL
Description	1-1	(18( Seq	Ä	3ARA) 601	70 GLDQ1       GLDQ1 670	140 PRSDDD0 
	-410	6-1	:у =	HPEI	SAIL SAIL	14( STPRSI        STPRSI 740
a E	-235	5-41 5-41	ore entit	x 10 50 30 40 50 50 20 30 40 50 0EOSLLRHSVTNSOLGSPAPGRHDRTLSRAGSDADGDSRSDSPLPHFRGKDS	60 10 120 DWFYARREAASAILGLDOKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDN	130 140 150 160 170 180 x FSLDTAITMPGTRSDDGDALFEGDKKSKQDASNVDVEELRQQAQMEEALKTAKQEF
e Na	s-09	9-23 9-23	Scc Ide tion	DFH1	YARR 1111 YARR 660	130 LDTAI        LDTAI 730
Sequence Name	1. US-09-235-416-1 Sequence 1, Application US	1. US-09-235-416-2 (1804-2352) US-09-235-416-1 Sequence 1, Application US/09235416A	Initial Score = Residue Identity = Gaps = Translation Frame	11.6	DWF       DWF	FSL 111 FSL
Seq		ä	Init: Resid Gaps Trans			
						•

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Frame

Sig.

Opt. Score

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-0.39 -0.40 -0.41 -0.41

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21 17 14 12

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FastDB

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Release 5.4

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Z D Z M W K

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CGTAAAAGFGGCAAAACTATTATGGATGGCCCGAAGGCATTTGCGTTCGATCGGTCGTATTGGTCCTTTGAC
CGTAAAAGTGCCAAAACTATTATGGATGGCCCGAAGGCATTTGCGTTCGATCGGTCGTATTGGTCGTTTTAC
150 170 180 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Significance
Mismatches
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2352
                                                                                         Length
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30
30
23
                                                                                                                                                                                                                                                        (1-1071)
Sequence 2, Application US/09235416A
                                                                                                                                                                                                                                                                                                            Optimized Score = 1071
Matches = 1071
Conservative Substitutions
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                                        13:
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   Sequence
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                                    best scores
                                                                                             Description
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100%
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1. US-09-235-416-2
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                                                                                                                                                                                                                                                        US-09-235-416-2
US-09-235-416-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230
                                      other
                                                                                                                                                                                                                                                                                                              Initial Score
Residue Identity
Gaps
                                                                                             Name
                                    The list of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510
                                                                                           Sequence
                                                                                                             Jul 102 15:23:47-PDT
                                                                                                                                                                                                                                         US-09-235-416-2 (1-1071) with:
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                                                                                                             bobryen
                                                                                                                                                                  (1-1071)
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Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714
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                                                                                                             рy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATISTICS
                                                                                                                                                              Query sequence being compared:US-09-235-416-2
Number of sequences searched:
Number of scores above cutoff:
                                                         Sequences
                                                                                                             made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
595
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15
                                                                                                                                                                                                                                       of the initial comparison of : USO9235416A.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2486
                                                                                                             Results file us-09-235-416-2-1-1071.res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARAMETERS
                                                         οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1476
                                                         Pairwise Comparison
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00:00:00:00
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of sequences searched:
of scores above cutoff:
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190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
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   IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity matrix
Mismatch penalty
Gap penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                         Results of
File : US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
```

-0

SHODEZOHS

SCORE

Sig. Frame

Init. Opt. Length Score Score

query sequence was found

sequence to the

A 100% similar

The scores be Significance

Number of Number

Scores

Times:

Description

Sequence Name

200

570

us-09-235-416-2-1-1071.res

```
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 | 690 | 690 | 690 | 700 | 710 | 720 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 690 | 710 | 710 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 
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580 630 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 810 820 830 840 850 860 GCAACGTCCACCGGGGGCTGCAGCTCTACGACCTA
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```

-0.39 0 21 Significance = 21 Mismatches = 10ns = 1 US-09-235-416-2 (1-1071) US-09-235-416-3 Sequence 3, Application US/09235416A Optimized Score = 21
Matches = 21
Conservative Substitutions X 10 X 30 40 ATGTCGGGCGGTGGAAATATCAAGGTGGTGGTGCGGGTACG 21 100% 0 0 0 8 Initial Score Residue Identity Gaps

AACCACGCAGT 1090

800 810 820 830 840 X 850 860 CGTCCACCGAGAGTCAACCGCTCACTTTCGACCTAGG Significance = Mismatches = = (1-1071) Sequence 6, Application US/09235416A Optimized Score = 17
Matches = 17
Conservative Substitutions 17 408 0 ( US-09-235-416-2 US-09-235-416-6 0 1 9 Initial Score Residue Identity Gaps

-0.40 13

US-09-235-416-2 (1-1071) US-09-235-416-5 Sequence 5, Application US/09235416A 4.

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-0.41
9
0
                                    -0.41
15
0
                                                                                                                                                                   -0.42
9
   . .
                                                                                                                                                                                                                                                                                                  290 300 X 310 320 X 330 AATGCATTCAAGGGTTGGGGAAGTCCT
                                                                                                                                                                                                                                                              Optimized Score = 11 Significance
Matches = 14 Mismatches
Conservative Substitutions
  Significance
Mismatches
                                                                                                                                Optimized Score = 15 Significance
Matches = 15 Mismatches
Conservative Substitutions
                                                                                                     US-09-235-416-2 (1-1071)
US-09-235-416-7 Sequence 7, Application US/09235416A
                                                                                                                                                                                                                                    (1-1071)
Sequence 4, Application US/09235416A
 Optimized Score = 21
Matches = 21
Conservative Substitutions
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368
0
14
538
0
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58%
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                                                                                                                                                                                                                                  US-09-235-416-2
US-09-235-416-4
Initial Score
Residue Identity
Gaps
                                                                                                                               Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                             Initial Score
Residue Identity
Gaps
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- Fast

FastDB

Results file Release 5.4

50-

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0 4

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60 70 80 90 100 110 120 CCAAGACGAGGAGAGCGCGCTCGAGGAGTTCAGCATCGAAAAGGGCT
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Score
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Mismatches
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14 Mismatches
                                                                             Init.
Score
                                                                                                                                  11
8
5
       477
     2352
                                                                                              Length
                                                                                                                                30
21
23
                                                                                                                                                                                                                                         (1327-1803)
Sequence 2, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1327-1803)
Sequence 7, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                      30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score = 14
Matches = 14
Conservative Substitutions
                                                                                                                                                                                                                                                                                            Optimized Score = 477
Matches = 477
Conservative Substitutions
     ns
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us
us
                                                                                                                                Application
Application
Application
Application
     Sequence 2, Application
                                                                                                                              7,96,4
                                                                                                                          US-09-235-416-7 Sequence US-09-235-416-6 Sequence US-09-235-416-3 Sequence US-09-235-416-4 Sequence
                                       best scores
                                                                                              Description
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0
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100%
0
   1. US-09-235-415-2
                                                                                                                                                                                                                                       US-09-235-416-2
US-09-235-416-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-235-416-2
US-09-235-416-7
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                                       other
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Residue Identity =
Gaps
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1820
                                                                                                                                                                                                                                                                                            Score
Identity
                                                                                              Маше
                                       The list of
                                                                                              Sequence
                                                                                                                                                                                                                                                                                            Initial Residue
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N
                                                                                                           Tue 23 Jul 102 15:24:40-PD
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                                                                                                                                                                                                                                      US-09-235-416-2 (1327-1803) with:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Init. Opt.
Length Score Score
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30
477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Standard Deviation 191.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total Elapsed 00:00:00:00
                                                                                                             bobryen
                                                                                                                                                              (1327-1803)
6
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-tuple
Joining penalty
Window size
                                                                                                             ρχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The scores below are sorted by initial score. Significance is calculated based on initial score
                                                                                                             made
                                                      Sequences
                                                                                                                                                              Query sequence being compared:US-09-235-416-2
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATISTICS
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7
                                                                                                         us-09-235-416-2-1327-1803.res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2486
                                                                                                                                                                                                                                    Results of the initial comparison File: US09235416A.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARAMETERS
                                                      Comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPU
00:00:00.00
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0.33
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85
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scores above cutoff:
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                                                      Pairwise
IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues:
```

53-

SCORE

100% similar

of of

Number Number Number

Scores

Times:

Sequence Name

3. US-09-235-416-2 (1327-1803) US-09-235-416-6 Sequence 6, Application US/09235416A

8 Optimized Score = 15 Significance = -0.40 33% Matches = 15 Mismatches = 15 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

4. US-09-235-416-2 (1327-1803) US-09-235-416-3 Sequence 3, Application US/09235416A

Initial Score = 6 Optimized Score = 9 Significance = -0.41
Residue Identity = 42% Matches = 9 Mismatches = 12
Gaps = 0 Conservative Substitutions = 0

40 x 80 90 cagactiggccargacaggaaatccacaaggaagggggggc ATGTCGGCGGTGGAAATATC X 10 20

5. US-09-235-416-2 (1327-1803) US-09-235-416-4 Sequence 4, Application US/09235416A

5 Optimized Score = 12 Significance = -0.42 52% Matches = 12 Mismatches = 11 0 Conservative Substitutions = 0 Initial Score = Residue Identity = Gaps

Frame

0

- Fast Pairwise Comparison of

Release 5.4

FastDB

Results of File : US

100-

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SECRECES

IntelliGenetics

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| 350 | 360 | 370 | 380 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 70 80 90 110 120 CTGCTCCAGGGCTCGGACGGGACGGGATCTCCGGTTCGGATT
                                                                                                                                                                                                                                                                                                                                                                                                2.04
                                                                                                                                                                                       -0.38
-0.40
-0.41
     2.04
                                                                                                                                   Sig.
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                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score - 549 Significance - 549 Mismatches - 549 Mismatches - Conservative Substitutions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 510 510 520 530 540 X TTGAGGAGGTTGCGTCAACAGCGAAGCAGGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Opt.
Score
     549
                                                                                                             Init.
Length Score
     549
                                                                                                                                                                                          15
9
     2352
                                                                                                                                                                                                                                                                                                                1. US-09-235-416-2 (1804-2352)
US-09-235-416-2 Sequence 2, Application US/09235416A
                                                                                                                                                                                       30
23
21
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US-09-235-416-7 Sequence 7, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
1. US-09-235-416-2 Sequence 2, Application US
                                                                                                                                                                                       us
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us
                                                                                                                                                                                     7, Application t
4, Application t
3, Application t
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                                                      13:
                                                                                                                                                                               US-09-235-416-7 Sequence US-09-235-416-4 Sequence US-09-235-416-3 Sequence
                                                      The list of other best scores
                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290
                                                                                                                                                                                                                                                                                                                                                                                                  549
100%
0
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                                                                                                                                                                                                                                                                                                                                                                                                        H O H
                                                                                                                                                                                                                                                                                                                                                                                                Initial Score
Residue Identity
                                                                                                                                      Sequence Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                      Results file us-09-235-416-2-1804-2352.res made by bobryen on Tue 23 Jul 102 15:25:18-pd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sig. Frame
                                                                                                                                                                                                                                                                                                                                            3 of the initial comparison of US-09-235-416-2 (1804-2352) with:
USO9235416A.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Init. Opt.
Length Score Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Standard Deviation 220.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total Elapsed 00:00:00.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                                                                 Ouery sequence being compared:US-09-235-416-2 (1804-2352)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A 100% similar sequence to the query sequence was found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEARCH STATISTICS
                                                                               Sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Median
8
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PARAMETERS

5.00 -0

Gap size penalty Cutoff score Randomization group

Unitary

Similarity matrix Mismatch penalty

Gap penalty

1244

183

122

61

SCORE

2486 6 6

Number of residues: Number of sequences searched: Number of scores above cutoff:

Description

Sequence Name

CPU 00:00:00.00

Mean 98

Scores

Times:

4. US-09-235-416-2 (1804-2352) US-09-235-416-3 Sequence 3, Application US/09235416A Sig. Frame

0

1.80

0.50 -0.30 -0.40 -0.80

FastDB

v 0

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TTTGAAAATGTGGACAACGTTGTGACCATGTGCAAACGAGGAGGCTGCTGTCATGTGAACGGCGTGCGA
1640 1650 x 1660 1670 1680 1690 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 70 80 90 100 CGCAA------CTCCTCAACATTAGACGCATCCTG-----ATTCGACTTCTT-----AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 220 | 330 | 340 | 350 | 360 | 370 | 380 | 370 | 380 | 370 | 102 | 102 | 102 | 102 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 | 103 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X 10 20 30 40 50 GAATTCCTGCTTCGCTGTTTTCAGGGCTTCTTCCATCTGAGCCTGCTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atagaaccagtcgctatcctttccacgaaagtgcggcaaagagagaatctgagcgagaatcgc - - cgtccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 180 230 230 230 CGAGCGAGAAATTATCGAGCGAGAAACGAACGAATCGCGAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Init. Opt.
Length Score Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Significance
Mismatches
                                                                                1. US-09-235-416-2 Sequence 2, Application us 2352 36 **** 2. US-09-235-416-4 Sequence 4, Application US 2352 36 3. US-09-235-416-5 Sequence 6, Application US 23 23 3. US-09-235-416-5 Sequence 7, Application US 30 15 5. US-09-235-416-3 Sequence 7, Application US 30 14 5. US-09-235-416-3 Sequence 3, Application US 30 14

    US-09-235-416-2' (1-1071)
    US-09-235-416-2 Sequence 2, Application US/09235416A

                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score = 246
Matches = 298
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
408
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
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Residue Identity
Gaps
                           Sequence Name
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                                                                                                                                                                                                     by bobryen on Tue 23 Jul 102 15:26:17-F
                                                                                                                                                                                                                                                                                                                                                                                                              Results of the initial comparison of US-09-235-416-2' (1-1071)
File : US09235416A.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
477
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00:00:00.00
                                                                                                                                                                                                                                                                                  Query sequence being compared:US-09-235-416-2' (1-1071)
Number of sequences searched:
Number of scores above cutoff:
6
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                                                                                                                  Pairwise Comparison of Sequences
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Cutoff score
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sequences s
                                                                                                                  - Fast
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N M O D M Z O M N

|| | | | | | ---AAGAAGTCG 2260

GAATGGCGAAGCAAGGATTGTTCTTGCCGTTCCGCACGAGCTTCTTCCGGATGGTTGAATCGAAAAATGTGG

550

540

A 100% identical sequence to the query sequence was not found

of of

Number Number

Scores:

SCORE

The list of best scores is:

us-09-235-416-2-inv-1-1071.res

```
23 Optimized Score = 23 Significance = 0.50 100% Matches = 23 Mismatches = 0 0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 Optimized Score = 16 Significance = -0.30
40% Matches = 16 Mismatches = 14
0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 Optimized Score = 15 Significance = -0.40
36% Matches = 15 Mismatches = 15
0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 Optimized Score = 10 Significance = -0.80 47% Matches = 10 Mismatches = 11 0 Conservative Substitutions = 0
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    US-09-235-416-2' (1-1071)
    US-09-235-416-4 Sequence 4, Application US/09235416A

                                                                                                                                                                                                                                                                                                                                                                                                           3. US-09-235-416-2' (1-1071)
US-09-235-416-6 Sequence 6, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4. US-09-235-416-2' (1-1071)
US-09-235-416-7 Sequence 7, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5. US-09-235-416-2' (1-1071)
US-09-235-416-3 Sequence 3, Application US/09235416A
                                                                                                                                                                                                                                                                                                         ATGTCGGCCGTGGAATATC x 20
                                                                                                                                     Initial Score Residue Identity Gaps
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Release 5.4

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Sig. Frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAGCTGGCCAAGGAAATCCACAAGGAACGAGGGGGGGCGCTCGAGGGGCTGGGTATCAGCATC 1370 1420 1430 1440
                                                                                                                                                                                                                                                                                                                                                                              GTACTGACGTGGCTTCTGAAGGACTCCTTGGGAGGCAACTCGATGACGGCCATGATTGCCGCCTTTTCGCCT
950 1000 1100 1100
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                                                                                                                                                                                                                                                       Optimized Score - 179 Significance - 1.97
Matches - 206 Mismatches - 265
Conservative Substitutions - 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 Significance - 0.00
Length Score Score
                                                                                   113
                                **** 1 standard deviation above mean ****
                                             US-09-235-416-2 Sequence 2, Application US 2352 34
**** 0 standard deviation from mean ****
US-09-235-416-7 Sequence 7, Application US 30 14
US-09-235-416-6 Sequence 6, Application US 30 12
US-09-235-416-5 Sequence 5, Application US 30 9
US-09-235-416-4 Sequence 4, Application US 23 8
US-09-235-416-3 Sequence 3, Application US 23 8
                                                                                                                                                                                                      US-09-235-416-2' (1327-1803)
US-09-235-416-2 Sequence 2, Application US/09235416A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-235-416-2' (1327-1803)
US-09-235-416-7 Sequence 7, Application US/09235416A
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CACGTAGGGGCCGGT
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Sequence Name
                                                                                                                                                                                                                                                           Initial
                                                                                 Results file us-09-235-416-2-inv-1327-1803.res made by bobryen on Tue 23 Jul 102 15:26:
                                                                                                                                                                                                                       Results of the initial comparison of US-09-235-416-2' (1327-1803) with: File : US09235416A.seq
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                                                                                                                                                  Query sequence being compared:US-09-235-416-2' (1327-1803)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-tuple
Joining penalty
Window size
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                                                - Fast Pairwise Comparison of Sequences
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191

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SCORE

PARAMETERS

5.00 Unitary 1

Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group

Median 10

Mean 14

Scores:

CPU 00:00:00

2486 6 6

Number of residues: Number of sequences searched: Number of scores above cutoff:

The list of best scores is:

A 100% identical sequence

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43% Matches = 17 Mismatches 0 Conservative Substitutions
Residue Identity - Gaps
```

3. US-09-235-416-2' (1327-1803) US-09-235-416-6 Sequence 6, Application US/09235416A

12 Optimized Score = 19 Significance = -0.20 50% Matches = 19 Mismatches = 11 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

4. US-09-235-416-2' (1327-1803) US-09-235-416-5 Sequence 5, Application US/09235416A

9 Optimized Score = 13 Significance = -0.49 30% Matches = 13 Mismatches = 17 0 Conservative Substitutions = 0 Initial Score = Residue Identity = Gaps

5. US-09-235-416-2' (1327-1803) US-09-235-416-4 Sequence 4, Application US/09235416A

8 Optimized Score = 12 Significance = -0.59 52% Matches = 12 Mismatches = 11 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

6. US-09-235-416-2' (1327-1803) US-09-235-416-3 Sequence 3, Application US/09235416A

7 Optimized Score = 10 Significance = -0.69 47% Matches = 10 Mismatches = 11 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

ATGTCGGCGGTGGAAATATC X 20

Frame

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-0.29 -0.29 -0.36 -0.51

Release 5.4

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120 136 180 180 180 180 180 180 CCTTCTGCAGTTCATGCCTTGCCAT AATTTAATAATGCCTGGGAAATCGGGGGATCACGCCATGCTCCTTGCCAT AAATTTACAATGAACAAGTGGG ------AGACTTGCTGAATGCGTCGACAAAGGGGAATCTAAGGTCG 520 520 530
                                                                                                                                                                                                                                                                                             CCGGTTCGGGCAAGTCCTATTCATGATGATAAGAGAAGAGCATGGCGAGGATTTGCCAGG
330 340 380 350 350 400
                                                                                                                                                                                                                                                                                                                                                                                                                       CCACGCCGTCTTCACTTTGACGCAAAAGTGGCATGATGAGGGGCCAAAATGGACACAGGAAGGT 750 750 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGCCATCCA---TAATAGTTTTGCCACTTT---TACGCGCCTTCTTCGGCACCCGGAGGGGGTGAG
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Init. Opt.
Length Score Score
                                                                                                                                                                                                                                   Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     460
                                        US-09-235-416-2 Sequence 2, Application US 2352 42 **** O standard deviation US 2352 42 **** O standard deviation From mean **** US-09-235-416-4 Sequence 4, Application US 23 10 US-09-235-416-7 Sequence 6, Application US 30 10 US-09-235-416-7 Sequence 3, Application US 30 9 US-09-235-416-3 Sequence 3, Application US 30 9 US-09-235-416-3 Sequence 3, Application US 21 7
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                                                                                                                                                                                   1. US-09-235-416-2' (1804-2352)
US-09-235-416-2 Sequence 2, Application US/09235416A
                                                                                                                                                                                                                                Optimized Score - 210
Matches - 251
Conservative Substitutions
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                Sequence Name Des
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Residue Identity
Gaps
                                                                                        26.4.2
                                                                                                         by bobryen on Tue 23 Jul 102 15:27:3
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477
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Joining penalty
Window size
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                                                                                                                                                   compared: US-09-235-416-2'
                                                                                                       Results file us-09-235-416-2-inv-1804-2352.res
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                                                           Sequences
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                                                           - Fast Pairwise Comparison of
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scores above cutoff
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              IntelliGenetics
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Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- 10
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SCORE

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query sequence was not found

the

A 100% identical sequence to

of of

Number

Scores:

Times:

best scores is:

The list of

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10 Optimized Score = 13 Significance = -0.29
56% Matches = 13 Mismatches = 10
0 Conservative Substitutions = 0

    US-09-235-416-2' (1804-2352)
    US-09-235-416-4 Sequence 4, Application US/09235416A

                                           Initial Score
Residue Identity Gaps
```

3. US-09-235-416-2' (1804-2352) US-09-235-416-6 Sequence 6, Application US/09235416A

10 Optimized Score = 15 Significance = -0.29 36% Matches = 15 Mismatches = 15 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

GCGCGAATTCTCDGANCCDGCVARRTCNAC x 30

4. US-09-235-416-2' (1804-2352) US-09-235-416-7 Sequence 7, Application US/09235416A

9 Optimized Score = 16 Significance = -0.36 36% Matches = 16 Mismatches = 14 0 Conservative Substitutions = 0 Initial Score = Residue Identity = Gaps S.\_TUS-09-235-416-2' (1804-2352) US-09-235-416-3 Sequence 3, Application US/09235416A

7 Optimized Score = 11 Significance = -0.51 52% Matches = 11 Mismatches = 10 0 Conservative Substitutions = 0 Initial Score Residue Identity Gaps

W89640 mf75c03.rl AW844305 RC4-CN005 R56708 y1044h08.rl BF028620 601763846 AA773267 af82f03.r

AW304933 xv97c10.x AI726774 BMCHGH652 BF115925 7n74g10.x BG926285 HNC33-1-D AW131625 xf32c08.x BG329673 602429286 BF096178 MR3-0T009

BG082824 H3081B06-AI730423 BNLGH1714 BM311296 1463406.x BE540124 601061039 BH033255 RPCI-24-2

H94360 yw54c08.rl BE764542 PM4-NT007 W06924 za90b10.rl

AW027726 W475F0120 AA206424 Zq58F08.5 B1858782 G03386385 B1335414 G02997992 AA396274 AA396274 BE612911 G01458181 AL571242 AL571242

DB sed DB sed

Minimum I Maximum I

Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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AZ390315

396 bp DNA linear GSS 03-OCT-200
1M0151C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0151C07 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus subtractos; Chordata; Cranlata; Vertebrata; Euteleostoml; Bukaryota; Metazoa; Chordata; Ciurognathi; Muridae; Murinae; Musmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396)
Dunn, D., Aoyaqi, A., Barber, M., Meacorn, T., Duval, B., Hamil, C., Aoyaqi, A., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .396 /-
/organism="Mus musculus"
/strain="C57BL/6J"
/baref="taxon:10090"
/clone="UUGC1M0151C07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0151 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
W89640
AW844305
R56708
BF028620
AA773267
                                                                                                H94360
BE764542
W06924
BC082824
AI730423
BM311296
BE540124
BE340124
BE115925
BG72628
AW131625
BG32673
BG32673
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BF0366178
AW027726
BANO6424
BISS782
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Fax: 801 585 7177
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  VERSION
KEYWORDS
SOURCE
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AUTHORS
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  AZ804125 IM0151C07
AZ804429 ZM0065H14
AZ685448 ENTJYITF
AAZ53238 ZF53E07.r
AW844301 RC4-CN005
TO6084 EST93973 Fe
AAJ78449 EST91145
AAJ5571 EST6433
AAJ5571 EST6433
AAJ5620 ZD71E02.r1
BE845084 CM1 HT114
AQZ60577 CTPB1-E1-
BIO33412 PM1-NN120
AVZ1381 AYZ1381
BE995757 MR2-GN01Z
AQ333260 HS_S002A
                                                                                                                                 July 25, 2002, 04:39:12; Search time 2969.55 Seconds (without alignments) 104.538 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                              27472414
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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AW844294
AA435871
AA411640
W25620
BF845084
AQ260557
BIO33412
AV721381
AQ333260
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em_gss_inv:*
em_gss_pln:*
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length: 2000000000
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23
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gb_htc:*
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GSS 03-OCT-2000

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Score

Result

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167
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            //decimingtore contribution and constant velocity. The bina was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|q'32114|qb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for ampicillin resistance."

selectred for ampicillin resistance."
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AZ804429.1 GI:12956752
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Run. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.7%; Score 18.8; DB 12; Length 396; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 2; Indels 0;
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Insert Length: 10000 Std Error:
Plate: 0065 row: H column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0065H14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GAATTCCTGCTTCTCTGGTTTC 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
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COMMENT
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KEYWORDS
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RESULT

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qil47321141gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOSI; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9208
Tel: 301 838 344 845
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 882)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 4.5e+02;
0; Mismatches 2; Indels 0;
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High quality sequence stop: 766.
Location/Qualiflers
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573 ATTTCCTGCTTCGCTGTTTTAA 594
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Seq primer: M13-Forward
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90.98;
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Best Local Similarity 90.9
Matches 20; Conservative
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Best Local Similarity
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LOCUS
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1 (bases I to 178)
Hillier,L., Allen, Bowles,L., Dubuque,T., Geisel,G., Jost,S., Rucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Washu-Marck EST Project 1997
Conpublished (1997)
Conpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-Torgan: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHW, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of
using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA253238 178 bp mRNA linear EST 06-AUG-1997 zz53f07.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667141 5' similar to TR:G1063396 G1063396 RAGA. ;, mRNA sequence.
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/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Lengh: 598 Std Error: 0.00
Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 1.
Localion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                           Length 882;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                         Score 18.8; DB 12;
Pred. No. 4.5e+02;
D; Mismatches 2;
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/organism="Homo sapiens"
/db_xref="GDB:5561108"
/db_xref="taxon:9606"
/clone="IMAGE:667141"
                                                                                                                                                                                                                                                                                                                                                                                                                                           722 AATTCTTGCTTCACTGTTTTCA 743
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90.9%;
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Best Local Similarity
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ORIGIN
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AUTHORS
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AWB44301 224 bp mRNA linear EST 18-MAY-2000 RC4-CN0050-130200-012-f01 CN0050 Homo sapiens cDNA, mRNA sequence. AWB44301
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 224)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., W.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-CN0050-130
200-012-f01&t3=2000-02-13&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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O
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 224;
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                                                                                                                                              Score 18.2; DB 9;
Pred. No. 6.8e+02;
); Mismatches 3;
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Pred. No. 7e+02;
0; Mismatches
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/db_xref="taxon:9606"
/clone_lib="CN0050"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 22
High quality sequence stop: 224.
Location/Qualifiers
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87.08;
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ilarity 87.0%;
Conservative
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79.1%; Scc. 87.0%; Pred 0;
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Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                 Bioinformatics
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1 (bases 1 to 281)

Adams.M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O.S., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,
                                                                                                                                T06084 280 bp mRNA linear EST 30-JUN-1993 EST03973 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDO22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA378449 28T 21-APR-1997 EST91145 Synovial sarcoma Homo sapiens cDNA 5' end similar to guantine nucleotide-binding protein ragA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="ATCC (inhost):82755"
/db_xref="ATCC (inhost):82755"
/clone="HFB0202"
/clone="HFB0202"
/clone="HFB0202"
/clone="Lose in Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, female; oligo-dT + random primed cDNa synthesis; lambdaZAP-II
vector, 1.0k average inser size."

4 c 60 g 80 t 10 others
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherlai; Primates; Catarrhini; Hominidae; Homo. 1 (bass 1 to 280)
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
Adams, M.D., Rerlavage, A.R., Fields, C. and Venter, J.C.
At 400 expressed sequence tags identify diversity of transcripts from human brain
Nature Genet. 4, 256-267 (1993)
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Pred. No. 7.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Adams, MD
The Institute for Genomic Research
32 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699423
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GAATTCCAACTTCGCTGCTTTCA 166
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1 gaattcctgcttcgctgttttca 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA378449
AA378449.1 GI:2030768
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87.0%;
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Best Local Similarity
Matches 20; Conserv
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T06084
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Kelley,J.C., Llu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
Wenter,J.C.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 293)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 7.2e+02;
); Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="synovial membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="ATCC (inhost):182850"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Synovial sarcoma"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 306)
1 (bases I to 306)
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1 (bases I. to 306)
1 (bases I. to 306)
2 (bases I. to 306)
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4 (
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                                                                                                                                                                                                                                        The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
19712 Medical Center Drive, Rockville, Rockv
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/db_xref="CDB:5576564"
/db_xref="taxon:9606"
/db_xref="IAGE:73700"
/clone="IAGE:73700"
/clone=lib="Soares_NhiMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RN
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: est@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="Amcc (inhest):157999"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
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87.0%; Pred. No. 7.3e+02;
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 t
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/organism="Homo sapiens"
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                                                                                                               Other_ESTs: THC189208
Contact: Kerlavage, AR
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1. (bases 1 to 303)

2. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

3. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

3. C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

3. O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mal, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

3. L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Glodek, A.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Felley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Rong, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, M.W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon,

Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="croN0050"
/dev_stage="Adult"
/note="Organ: colon_normal; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
10 a 81 c 64 g 72 t
                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-CN0050-130
200-012-c08&t3=2000-02-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence start: 9
Location/Qualifiers
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             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST64335 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to guanine nucleotide-binding protein ragA, mRNA sequence.
AA355871.1 GI:2008190
EST.
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Pred. No. 7.3e+02;
0; Mismatches 3; Indels
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Best Local Similarity 87.0%;
Matches 20; Conservative
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                        /lab_host="Corrections of the property of the 
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2b71e02.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:309050 5' similar to WP:T24F1.1 CE02361 GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 738 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 234.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 7.3e+02;
0; Mismatches 3; Indels (
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/db_xref="GDB:1252463"
/db_xref="taxon:9606"
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pregnant uterus"
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W25620.1 GI:1303455
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Best Local Similarity 87.0
Matches 20; Conservative
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1. .328
/organism="Homo sapiens"
/draw state="taxon:9606"
/dlone_lib="#T1145"
/dev_stage="Adult"
/dev_stage="Adult"
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/note="Organ: head_neck; Vector: pucl8; Site_l: Smal; Site_l: Smal; Site_l: Smal; A mini-library was made by cloning products Site_l: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA amplification were performed under low stringency conditions.

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvallo, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMIst2=CMI-HT1145-
271200-677-d008t3=2000-12-27st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 327.
High quality sequence stop: 327.
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHH19W."
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CMI-HT1145-271200-677-d08 HT1145 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                     Score 18.2; DB 10; Length 322;
Pred. No. 7.3e+02;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                     79.1%;
87.0%;
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local S
Matches 20
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lbb="NN1207"
/dev_stage="Adulto"
/note="Organ: nervous_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Gerived from ONESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under low stringency conditions.
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                           Homo sapiens
Bukaryota; Mactazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.J.r., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FOLIOWing URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMI&t2=PM1-NN1207-
150201-023-b07&t3=2001-02-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 317.
                                                                                                                                                                                                                                                                                                                   Shofgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 bp mRNA linear EST 16-OCT-2 AV721381 HTB Homo sapiens cDNA clone HTBADE08 5', mRNA sequence. AV721381.1 GI:10818533 RSM
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Pred. No. 7.4e+02;
); Mismatches 3;
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87.08;
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Other_GSSs: CIPBI-E1-2508E24.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3.21
Class: BAC ends.
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Homo sapiens CDNA, mRNA sequence.
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BC Library D"
67 c 75 g 97 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 3;
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/db_xref="taxon:9606"
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EST 16-OCT-2000

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Gaps

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Contact: Zequang Han
Contact: Zequang Han
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, p. R. China
Tel: 86-21-50801922
Email: hanzgérhgc.sh.cn
This clone is available at CHGC in Shanghai.

Location/Qualifiers
Ince / Organism="Homo sapiens"
/ db_xref="taxon:9606",
/ clone="HTBPERDE"
/ clone="HTBPERDE"
/ tissue_type="Hypothalamus"
/ dev_strage="#Adult"
/ loce="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Leishmania chagasi Drosophila melanog Drosophila melanog Human protein SEQ Human protein SEQ Drosophila melanog Amino acid sequenc

Homo s (491. S

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KSP-S553. KSP-K491 Human KSP. Human KSP-K

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Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease

Goldstein LSB, Sakowicz R;

Human kinesin-like Drosophila melanog Human diagnostic a Drosophila melanog Gene 5 human secre Human secreted pro Human polypeptide

AAU19569 ABB62962 AAB63189 AAB63190 AAM41820

441.1 441.1 440.1 335.5 31.7

4030 1668.5 1660.5 1658 1658 1658 1635 1430 1396.5 1278.5

100.0

Score

Result Š

WPI; 1999-493950/41. N-PSDB; AAX87656.

This sequence represents Thermomyces lanuginosus TL-gamma, a novel arth-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family and kinesin superfamily. The invention provides TL-gamma nucleic acids (see AAX87656), proteins and antibodies, and methods of screening for TL-gamma modulators potentially useful for treating hyphal fungal infections and diseases caused by mutated TL-gamma, e.g. neurodegeneration involving anterograde axonal transport, such as Alzheimer's, parkinson's or Huntington's diseases or amyotrophic lateral sclerois. Detection of TL-gamma allows differentiation between hyphal and non-hyphal lungal infections. Score 4030; DB 20; pred. No. 1.8e-299; Query Match 100.0%; Score 4030; Best Local Similarity 100.0%; Pred. No. 1.8 Matches 784; Conservative 0; Mismatches 5; Page 70-71; 75pp; English. 784 AA; Sequence Claim ŏ g ò g 

420 480 240 300 360 61 afafdrsywsfdknapnyarqedlfqdlgvplldnafkgynncifaygqtgsgksysmmg 120 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180 240 Gaps 9 9 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS SIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISI NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGGPVEESYPPDTPLEKQIV 1 MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILLTPPPGAEEKARKSGKTIMDGPK 61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG HPSTGPYVEDLAKLVVRSFQE1ENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH ö Length 784; Indels 121 121 181 421 241 301 301 361 361 121 241 g q à ð g à g ò g ŏ ò 셤

FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNOTILTPPPGAEEKARKSGKTIMDGPKAFA 3 gasvkvavrvrpfnsretskeskciiqmqgnstsiinpknpke-----apksfs KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 21; Length 1816; Query Match
41.4%; Score 1668.5; DB 21
Best Local Similarity 45.0%; Pred. No. 3.5e-118;
Matches 356; Conservative 126; Mismatches 172; 1816 AA; Sequence 64 25 123 셤 ŏ g ò ò 540 540 900 GTIDNFSLDTAITMPGTPRSDDGDALFFGDKKSKQDASNVDVEELRQQQAQMEEALKTA 780 EKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK EHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAE RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN

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Indels 137; Gaps

Human; kinesin-like protein; HKLP; KIF1; cell division; cancer; intracellular transport; neurological disorder; infertility; biallelic marker; spontaneous abortion; neonatal chromosome disorder; An isolated or purified human kinesin-like protein (HKLP) encoc polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides -Human kinesin-like protein HKLP SEQ ID NO: ä English Grel Š AAB36227 standard; Protein; 1816 Bougueleret L, Dufaure-Gare I, Claim 46; Page 189-192; 199pp; 20-APR-2000; 2000WO-IB00562 99US-0130217 (first entry) WPI; 2000-665242/64. N-PSDB; AAC66550. WO200063375-A1 (GEST ) GENSET 784 781 kgef 784 Homo sapiens. 20-APR-1999; 19-FEB-2001 26-OCT-2000 aneuploidy KOEF AAB36227; 781 RESULT AAB36227 ò g

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DB 20;

The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFLA and KIFLB proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease diagnosis and population studies.

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PLEKQIVSIQQPDATVKKMS---------KAEIVEQLNQSEKLYRDLNQTW 455
                                                                Tang YT,
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Zhao QA,
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                                       432 MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH
HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
       AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG------GGAG----
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------tpsaetpsepvdwtfagrelle
                                DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM--
                                                                ---SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS
                                                                                                                                                                                                SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV-
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                                                                                                                                                                                                                                                                 SILRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAAS
                                                                                                                                                                                                                                                                                                665 AILGLDQK-----VQKARAVRGLVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 3179.
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2000US-0552317.
2000US-0598042.
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25-APR-2000;
09-JUL-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous cof the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous cof system, such as peripheral nervous system diseases, such as alzaeiner's, Parkinson's disease, Huntington's disease, amycrophic contilisation of the activities such as: Immune system suppression, contilisation of the activities such as: Immune system suppression, continually inhibit activity, chemotactic/chemokinetic activity, heemostatic and thrombolyzic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and continual activity arthritis and inflammation, leukaemias and continual activity arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                        for treating disorders
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Zhang J
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Yang Y,
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Conservative 126; Mismatches 167;
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. с. Xue AJ,
Drmanac RT;
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                                                                                                                                                                                       Chen R,
Xu C, 3
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Wehrman T, Xu
Goodrich R,
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wang Z, W
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                                                                                                                                         (HYSE-) HYSEQ INC
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  19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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KLIMP; kinesin-like motor protein; cytostatic; anticonvulsant; human; anti-Alzhelmer; anti-Parkinsonlan; antidabetic; anti-locerative; canoer; immunomodulatory; antiinflammatory; anti-AIDS; antitheumatic; treatment; antiarthritic; diagnosis; neurological disorder; vesicular transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel human kinesin-like motor protein (KLIMP) [1] which has cytostatic, anticonvulsant, anti-Alzheimer's, anti-Parkinsonian, antidiabetic, anti-Ucerative, immunomodulatory, antinflammatory, anti-AIDS, antirheumatic and antiarthritic activity. [1] and the protein it encodes may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate KLIMP expression such as cancers, neurological disorders and disorders of vesicular transport. For example, [1] (and vectors containing [1] [1V) and the KLIMP polypeptide may be used to treat disorders associated with decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences encoding a human kinesin-like motor protein (KLIMP) useful for the treatment of diseases associated with inappropriate KLIMP expression such as cancers, neurological disorders and disorders of vesicular transport -
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                                                                      IDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTL
                                                                                                                                                                                                                                                             629 SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV
                                                                                                                     KPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN-----VDNVVTIVPNEKAAVMVNGVR
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N-PSDB; AAZ44744.
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cancers of the breast lung and prostate), neurological disorders (e.g. epilepsy, Alzheimer's disease and Parkinson's disease), disorders of vesicular transport (e.g. diabetes mellitus/insipidus, Grave's disease and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g. acquired immune defliciency syndrome AIDS), rheumatoid arthritis and toxic shock syndrome). This sequence represents the human KLIMP protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                      123 K -- EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
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                                                                                                                                                               Length 1103
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                                                                                                                                                              Query Match 41.1%; Score 1658; DB 21; Best Local Similarity 47.3%; Pred. No. 1e-117; Matches 353; Conservative 120; Mismatches 159;
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                                                                    HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                         DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS
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                                                                                                                                                                                                                                                                                     NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGG-------
                                                                                                                                                                                                                                                                                                                                                          -----SGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                      Location/Qualifiers
97..104
/note= "ATP-binding site"
/lil..37
/label= Kinesin_motor_domain
/note= "This region is specifically referred in claim 1"
242..253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human kinesin-like motor protein (KLIMP) from Incyte clone 1281811. KLIMP and the corresponding polynucleotide are useful for diagnosis. treatment and prevention of disorders associated with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland), neurological disorders (such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, mental disorders), and disorders of vesicular transport (such as cancers), and disorders of vesicular transport (such as cytic fibrosis, diabetes mellitus, AIDS (Acquired Immune Deficiency Syndrome), viral, bacterial, fungal, helminthic, and protozoal infections).
                                                                                   leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; ischaemic cerebrovascular disease; stroke; Alzheimer's disease; blick's disease; dementia; Parkinson's disease; vesicular transport disorder: cystic fibrosis; diabetes mellitus; AIDS; Acquired Immune Deficiency Syndrome; microbial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequences encoding a human kinesin-like motor protein (KLIMP) useful for the prevention and treatment of diseases associated with inappropriate KLIMP expression such as cancers and neurological disorders
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                                                                    Human; kinesin-like motor protein; KLIMP;
                               Human kinesin-like motor protein (KLIMP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 37pp; English.
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N-PSDB; AAD08139.
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17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1773;
                                                                                                                                                                                         NO 18516; 21pp + Sequence Listing; English.
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                      2001-656860/75
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642 dt-----ggvdwnfagcellek-ggidlkaemkkrldnleegykreklgadggfeegr
                                              690 K---AR--AVRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMP-----
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Amshey S, Dahl CR, Dam TC, Daniels SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human diagnostic and therapeutic polypeptide (DITHP) #155.
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D'Sa SA, Amsi
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proceds in volved in growth and development and receptors. (I) and can divolved in growth and development and receptors. (I) and sasociated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, corpured into the deficiency syndrome (AIDS), lymphoma, and be used to produce the DITHPs, by inserting the nucleic acids in complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of cantibodies against DITHPs and in assays to identify modulators of DITHP captobe used to down regulate expression and activity. The anti-DITHP actibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant captobe the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant captobe to the presence of DITHPs in samples of the invention.
Jones AL;
, Daffo A;
                                                                                                                                                                                           Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
Fong WT, Greenawalt LB, Hillman JL, Jc
I, Rosen BH, Russo FD, Stockdreher TK, D
Yu JY, Bradley DL, Bratcher SR, Chen W;
I, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                               Claim 27; Page 488-490; 522pp; English
Dufour GE, Flores V,
Liu TF, Roseberry AM,
Wright RJ, Yap PE, Yu
Cohen HJ, Hodgson DM,
                                                                                                                        WPI; 2001-502867/55.
                                                                                                                                               N-PSDB; AAS31140
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17; GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTGK 238 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298 SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKR 358 IKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGPVEESYPPDTPLEKQ 418 63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121 Gaps 3 GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62 96; Length 757; Indels DB 22; Matches 321; Conservative 114; Mismatches 190; Score 1430; DB 22; Pred: No. 1.6e-100; 35.5%; Similarity Query Match Best Local 17 122 189 239 599 309 359 윱 셤 셤 ð 셤 g ò 셤 ö ö ð ð ò

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                       SIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKI
                                                                                                                                                                                                                               564 kkaerededqdpsmknensseq1------dvdgdsssevssevnf----
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; diagnosis; immunosuppressive; antiarthritic;
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                                  61;
                                  171; Indels
DB 22;
34.7%; Score 1396.5; DB 48.8%; Pred. No. 2.5e-97.1ve 88; Mismatches 17:
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The Arrivation of Arrivation of the Arrivation of the Arrivation of Arrivation of Arrivation and Arrivation of Arrivation and polypeptides homologous to them. Human secreted proteins have activities based on the tissues and cells the genes are expressed in.

Cathivities based on the tissues and cells the genes are expressed in. Camples of activities include: immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polymucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, also used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autonomine diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to also due to sunburn, to maintain organs before transplantation, for supporting cell outlure of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or the program of the parents of primary tissues, to regenerate tissues and in the exemplification of Arrestory the conditions of a pathological organs before transplantation of the program and the example of primary tissues, to regenerate tissues and in the exemplification of the arrest or discrete endocates expended as a food additive or the program and the condition of the arrest organs or decrease storage capabilities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 VREHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 1278.5; DB 21; Length 504; 50.9%; Pred. No. 3.4e-89; ive 77; Mismatches 144; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 487-488; 533pp; English
                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                           20-JAN-2000; 2000US-0176931.
                                                                                          06-APR-2000; 2000WO-US09071.
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Matches 274; Conservative
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                                                                                                                                                                                                                                                                              Ruben SM, Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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WO200061629-A1.
                                                                                                                                          09-APR-1999;
                                               19-0CT-2000
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins and polypeptides homologous to them. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; antiarthritic; antitheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; antiproliferative; dynostatic; cardiant; vasotropic; fungicide; and ophthalmological. The polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, malee, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fundicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebrou ischaemia; anglogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging;
                      KRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGPVEESYPPDTPLE 416
                                                                                                                           KQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEEL 476
                                                                                                                                                       GISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGS 536
                                                                                                                                                                                                                                                                13°
                                                                                                                                                                                                                                                                                                                                    537 KILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP 594
                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein sequence encoded by gene 5 SEQ ID NO:116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB63190 standard; Protein; 503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2000; 2000US-0176931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food additive; preservative.
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autoinmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypetides can also be used a food additive or preservative to increase or decrease storage capabilities. AAF22364 to AAF22372 and AAB63133 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GP-KAFAFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 YSMMGYGKEHGVIPRICQDMFRRI----NELQKDKNLTCTVEVSYLEIYNERVRDLLNP- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 AALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 IRLNGSKILKEHCTFE-NVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 STKGNLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTLTLTQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 VIAALADMSSGRQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 1276; DB 21; Length : 50.8%; Pred. No. 5.3e-89; ive 74; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41820 standard; Protein; 421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.8 Matches 277; Conservative
                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                                                                                                                                                                         503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594
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REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK
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                                                                                                                                                                                                                                                                                                                  pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interactions
                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                     ABB61704;
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression. Activinhibin activity, chemotactic/chemokinetic activity, heemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, as a sasys for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                              polypeptides, useful for treating disorders
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                                                                                                                                                                                                                                                                                            Zhang J;
                                                                                                                                                                                                                                                                                   Ren F,
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                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1251; DB 22;
; Pred. No. 3.3e-87;
68; Mismatches 64;
                                                                                                                                                                                                                                                                                   Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 6751; 10078pp; English.
                                                                                                                                                                                                                                                                                                         Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                          such as central nervous system injuries
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Wehrman T, Xu
Goodrich R, I
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61.1%;
                                                                                                                                                             2000US-0488725.
2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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Matches 245; Conserv
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Wang 2, V
Zhou P,
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                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                                        26-DEC-2000;
                                                                         Homo sapiens
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25-APR-2000;
                                                                                                                   26-JUL-2001
                                                    leukaemia.
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Wang J,
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                                                                                                     SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                                                                                                                                                                                                     WHDEETKMDIEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM
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11-JUL-2000; 2000US-0614150
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                                                               DKNLTCTVEVSYLEIYNERVRDLLNPSTKGN-LKVREHPSTGPYVEDLAKLVVRSFQEIE
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AKCIVRMEGNOTILTPPPGAEEKARKSGKTIMDGPKAFAFDRSYWSFDKNAPNYARQEDL
        FQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEHGVIPRICQDMFRRINELQR
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23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AITMPGTPRSDDDGDALFFGDKKSKQDASNV-----DVEELRQQQAQMEEALKTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 gglre-seeraaelasgleataaakssaegdrentratlegglres----earaael
GPKAFAFDRSYWSF - - - DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGK
                                                                                                                         SYSMMG-----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania chagasi; acidic ribosomal antigen; LCPO;
epitope; K39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
     : || ::::| |: |::::| 582 lrgqlaererelsragk-----swmeklkeaedgrkselrvlkrrglalel----ta
                                                                               750 dhpvdfglahgeilgkgegglrseleaekraaltkiegeraghardfeerlgclelegfk
                                                                                                                                                                                                                                                                                                      810 ykcnsemleterga----lalaqqqehtplrhedavstpaqkstiledigrimlnpsees
                                                                                                                              FENV - - DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP - - - EEARA
                                                                                                                                                                                                   ERQEQSLLRH----SVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDS-----PLPHFR
                                                                                                                                                                                                                                                                       650 GK-DSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKA---RAVRRGLVEDNEDS
                                                          SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVG-----NVNQDTQAEIRLNGSKILKEHCT
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Pred. No. 3.2e-53;
5; Mismatches 292;
                                                                                                                                                                                                                                                                                                                                             706 DSQSSFPVRD-----KYMSNGTIDNFSL 728
                                                                                                                                                                                                                                                                                                                                                                              866 lhktglmvkeatgrcrgldlplefrgtgtpdefgl 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide of Leishmania chagasi.
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Similarity 28.1%; Pr
33; Conservative 125;
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Query Match Best Local S1 Matches 253;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 NPSTKG-----NLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNM 220
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Best Local Similarity 28.1%; Pred. No. 3.2e-53;
Matches 253; Conservative 125; Mismatches 292; Indels 230; Gaps
                                                                                                                                                                                                                                                                                                                                                              New Leishmania acidic ribosomal P-protein family poly:peptide - used to develop prods. for diagnosis, detection and protection against Leishmania infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 36-43; 76pp; English.
                                                                                                                                                                     95US-0428414.
                                                                                                                               96WO-US05472
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Leishmania chagasi.
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Best Local Similarity 47.3%; Pred. No. 5.1e-131;
Matches 353; Conservative 120; Mismatches 159;
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Batterson, Chandra
TILE OF INVENTION: KINESIN-LIKE MOTOR PROTEIN
FILE REPERENCE: PP-0593 US
CURRENT APPLICATION NUMBER: US/09/162,373
CURRENT APPLICATION NUMBER: 1998-09-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PERL Frogram
SEQ ID NO 1
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US-08-353-700-1
US-08-353-700-1
US-08-328-254-6
PCT-US93-03077-1
US-08-685-871-2
US-09-104-3248-4
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; OTHER INFORMATION: 1281811
US-09-162-373-1
ORGANISM: Homo sapiens
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US-09-718-841-4
US-09-718-841-4
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US-09-572-191-2
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US-09-541-782-2
US-09-541-782-2
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US-09-722-139-2
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 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTKQIR 349
                                                                      -----SGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDL 451
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                                                                                                                                   VYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV-----DNVVTIVPNEKAAVMV
                                                                                                                                                                                    565 NGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRH
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Best Local Similarity 47.3%; Pred. No. 5.1e-131;
Matches 353; Conservative 120; Mismatches 159;
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Fatent No. 6248594
GRERAL INFORMATION
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GRERAL INFORMATION
FAPLICANT: Tang, Y. Tom
APPLICANT: Guesler, Karl C.
APPLICANT: Batterson, Chandra
TITLE OF INVENTION: KINESIN-LIKE MOTOR PROTEIN
FILE REFERENCE: PF-0593 US
CURRENT APPLICATION NUMBER: US/09/467,946
CURRENT FILING DATE: 1999-12-21
FARLIER APPLICATION NUMBER: 09/162,373
FARLIER PILING DATE: 1999-12-3
NUMBER: OF SEQ ID NOS: 2
SOFTWARE: PERL PROGRAM
                          NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGAGG-
                                                                                                                                                                                                                                                                                                                      685 FDDVQKARAVRRGLVEDNE---DSDS 707
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US-09-467-946-1
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Patent No. 635471

GREERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Freedman, Richard

TITLE OF INVENTION: No. 6355471el motor proteins and methods for

TITLE OF INVENTION: Library

TITLE OF INVENTION: Library

FILE REFERENCE: 1055

CURRENT APPLICATION NUMBER: US/09/722,139

CURRENT FILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 4

SOFT IN 0. 2

SOFT IN 0. 2
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Best Local Similarity 39.1%; Pred. No. 1.3e-101;
Matches 309; Conservative 117; Mismatches 241;
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us-09-235-416-1.rai

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GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL--NPSTKGNLKVR 179
                                                                                                                        EHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKW 239
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----KDLLAEKEKFEEERLREQO---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 -RAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 YARREAASAILGLDOKISHLTDDELDALFDDVQ---KARAVRRGLVEDNEDSDSQSSFPV
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Patent No. 633184

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6333184el motor prote;
FILE REFERENCE: 1051
CURRENT APPLICATION NUMBER: US/09/718,841

CURRENT FILLIGATION NUMBER: US/09/718,841

CURRENT FILLIGATION NOWBER: US/09/718,841

CURRENT FILLIGATION NOWBER: SOFORES OF TABLES OF TAB

    any amino acid

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OTHER INFORMATION: Xaa
NAME/KEY: VARIANT
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ORGANISM: Human
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                                                                                              Gaps
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Fatent No. 6355471
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6355471el motor proteins and methods for
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                                                                                                            GVIPRICODMFRRINELQKD---KNLTCTVEVSYLEIYNERVRDLLNPSTKG---NLKVR
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                                                                                             61;
                                                                   DB 4; Length 563;
                                                                                             Indels
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               amino acid
; LOCATION: (391)...(412)
; OTHER INFORMATION: Xaa = any
US-09-718-841-2
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                                                                                                                                                         56 FTYDESPYSADTKSPDYVSQEMVFKTLGTDVVKSAFEGYNACVFAYGQTGSGKSYTMMGN 115
                                                                                                                                                                                                     GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL--NPSTKGNLKVR 179
                                                                                                                                                                                                                           EHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKW 239
                                                                                                                                                                                                                                                                                        SG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD 354
                                                                   6 NIKVVVRVRPENAREIDRGAKCIVRMEGNQTILT----PPPGAEEKARKSGKTIMDGPKA 61
                                     Gaps
                                                                                       SVKVAVRVRPMNRREKDLEAKFIIQMEKSKTTITNLKIPEGGTGDSGRERIKT-----
   Length 359
                                   89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmaniasis
; Score 991; DB 4;
; Pred. No. 1.7e-75;
48; Mismatches 89
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ZIP: 98040-4906

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC COMPATABLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORD for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/006,676B

FILING DATE: 15-JAN-1993

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08006676B
Patent No. 5411865
GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Le
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATIONALIA DELLA DELLA BENERALIA DELLE DELLA BENERALION NUMBER: 32,585 REDERENCE/DOCKET NUMBER: REED-TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 232 7845 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jeffrey B. Oster
STREET: 8339 SE 57th Street
CITY: Mercer Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
       Query Match 24.6%;
Best Local Similarity 57.0%;
Matches 208; Conservative 41
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amino acid
3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AITMPGTPRSDDDGDALFFGDKKSKQDASNV-----DVEELRQQQAQMEEALKTAK 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASQLEATAAA-----KMSAEQDRENTRATLEQQLRDSEERAAELASQLESTTAAK 807
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480 raaalqeemtatrqadkmqalnlrlkeeqarkerellkemakkdaalskvrrrkdaeta 539
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                                                                                                                                                                                                                                                                                                                                                         ----SYPPDTPLEK 417
                                                                                                                                 SYSMMG-----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL 168
                                                                                                                                                                                       169 NPSTKG-----NLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNM 220
                                                                                                                                                                                                                                                                                    NETSSRSHAVFILIL----TQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLK 276
                                                                                                                                                                                                                                                                                                    249 NDRSSRSHAIIMLLLEERTWITKSGETIRTAGKSSRMNLVDLAGSERVAGSQVEGQQFK 308
                                                                                                                GPKAFAFDRSYWSF---DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGK 114
                                                       7 IKVVVRVRPFNARE--IDRGAKCIVRMEGNQTILTPP-----PGAEEKARKSGKTIMD 57
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                                                                               Indels 230;
   Length
20.2%; Score 814; DB 1; Lilarity 28.1%; Pred. No. 6.9e-60; Conservative 125; Mismatches 292;
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Patent No. 5719263
GENERAL INFORMATION:
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                     Similarity
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US-08-282-845-2
                        Best Local Sim
Matches 253;
         Query Match
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611 VINSQLGSPAPGRHDRILSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLD 670
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                                                                                                                                                    : ::|:
180 raaaloeemtatrroadkmoalnlrlkeeoarkerellkemakkdaalskvrrrkdaeta 539
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                422 -- AGGDPAYVSELKKKLALLESEAQKRAADIQALEREREHNQVQERLLRATEAEKSELES 479
                                                                                                                                                                                                                                                                                                                              540 SEREKL-----ESTVAQLEREQREREVALDAL------QTHQRKLQEALESSE 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              706 QQLRE-SEERAAELASQLEATAAAKSSAEQDRENTRATLEQOLRES-----EARAAEL 757
                                                                                                                                                                                                                                                        442 NQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSD 501
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GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: PErkins, Patricia Anne
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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-W
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
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COUNTRY: USA
                                                                                               418 QIVSIQQ----
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NETSSRSHAVFTLTL----TQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLK 276
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Best Local Similarity 28.1%; Pred. No. 6.9e-60;
Matches 253; Conservative 125; Mismatches 292; Indels 230; Gaps
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TITLE OF INVENTION: A 230kd Antigen Present in Leishmania TITLE OF INVENTION: Species NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101

ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System 7.1
COMPUTER: Microsoft Word for Macintosh 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
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NAME: PERKINS, PALTICIA AND
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-A
TELECOMMUNICATION INFORMATION:
TELEPAX: (206)587-0430
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUMRY 15, 1993
CLASSIFICATION: 435
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                   ISPADINFEETLSTLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PDATVKKMSKAEIVEQL 441
                                                                                                                                                                                  SYSMMG-----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL 168
                                                                                                            GPKAFAFDRSYWSF---DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGK 114
                                 Gaps
                                                                               7 IKVVVRVRPFNARE--IDRGAKCIVRMEGNQTILTPP-----PGAEEKARKSGKTIMD 57
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                                                                                                                                                                                                                                        189 GKRKKGVKGGGEEVYVDVREHPSRGVFLEGGRLVEVGSLDDVVRLIEIGNGVRHTASTKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3... Application US/08428414A

Sequence 1... Application US/08428414A

Patent No. 5912166

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: LEISHMANIASIS
  Length 955;
    Query Match 20.2%; Score 814; DB 5; Best Local Similarity 28.1%; Pred. No. 6.9e-60; Matches 253; Conservative 125; Mismatches 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 GGAGGSGGPVEE--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 NETSSRSHAVFTLTL----TQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGAEINRSLSTLGRVIAALADMSS-GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 IKVVVRVRPFNARE--IDRGAKCIVRMEGNQTILTPP-----PGAEEKARKSGKTIMD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 NDRSSRSHAIIMLLLREERTWTTKSGETIRTAGKSSRMNLVDLAGSERVAQSQVEGQQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 SYSMMG-----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
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40.0%; Pred. No. 9.2e-60;
tive 75; Mismatches 164;
                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                 Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kadlecek, Ann T.
REGISTRATION UNBER: 39,244
REFERENCE/DOCKET NUMBER: 210121.407
TELECOMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFAX: (206) 682-6031
TELEFX: 372385 SEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 21-APR-1995
CLASSIFICATION: 436
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                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                 E: SEED and BE
6300 Columbia
CORRESPONDENCE ADDRESS:
                                                                                Washington
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Best Local Similarity
                                                                                                    COUNTRY: USA
ZIP: 98104-7092
                                                              : Seattle
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                    ADDRESSEE:
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                                                                                                                                                                                                                                   SOFTWARE:
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FastSEQ for Windows Version 4.0
                                                 ; ORGANISM: H.sapiens
US-09-541-782-10
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SOFTWARE: Fast
SEQ ID NO 10
LENGTH: 1057
                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVIPRICQDMFRRINELQKD---KNLTCTVEVSYLEIYNERVRDLLNPSTKG---NLKVR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKW 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 HDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 ---SGKQKKN--QLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFD 65
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6333184el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1051
CURRENT APPLICATION NUMBER: US/09/718,841
CURRENT PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                  Length 357;
                                                                                                                                                                                                                                                                                                                                              18.5%; Score 747; DB 4; L
46.6%; Pred. No. 6.4e-55;
tive 54; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: NISLOW, COTEY
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
ITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT APPLICATION NOWBER: US/09/541,782
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (16)...(37)
OTHER INFORMATION: Xaa = any amino acid
                                                 Sequence 4, Application US/09718841
Patent No. 6333184
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.6%
Matches 170; Conservative
                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 SAKNI 356
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                                                                                                                                                                                                                   LENGTH: 357
                                     -09-718-841-4
                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                 Gaps
                                                                                                                                                                                                                                                      GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                                                                                                                                                                                                                                                                                                                                                    16 GKNIQVVVRCRPFNLAERKASAHSIVECD-----PVRKEVSVRTGGLADKSSRKTYT 67
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Query Match 16.7%; Score 673; DB 4; Length 1057; Best Local Similarity 27.1%; Pred. No. 6.4e-48; Matches 245; Conservative 146; Mismatches 290; Indels 224;
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SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFTLTLTQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLG 289
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                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                  TITLE OF INVENTION: No. 6355466el motor proteins and methods for TITLE OF INVENTION: No. 6355466el motor proteins and methods for TITLE OF INVENTION: Their use FILE REFERENCE: 1017
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                     Indels 227;
                                                                                                                                                                                                                                                                                                             Length 1388;
                                                                                                                                                                                                                                                                                                              Query Match 16.5%; Score 664.5; DB 4; Best Local Similarity 27.4%; Pred. No. 5.2e-47; Matches 258; Conservative 129; Mismatches 327;
                                                                  Sequence 2, Application US/09572191 Patent No. 6355466
                                                                                                         Beraud, Christophe
                                                                                          GENERAL INFORMATION:
APPLICANT: Beraud, Christop
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
|:| |
ESLNT 825
                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human
US-09-572-191-2
                                                                                                                                                                                                                                         LENGTH: 1388
                                                         US-09-572-191-2
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                               690 NSSILDNDILNE-PVPPEMNEQAFEAISEELRTVQEQMSALQAKLDEEEHKNLKLQQHVD 748
                                                                                                                                                                                                                              696 RGLVEDNEDSD---SQSSFPVRDKYMSNG------TIDNFSLDTAITMPGTPRSDD 742
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                                                                                                                                                                                                    ----H-----FRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVR
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TITLE OF INVENTION: No. 6355466el motor proteins and methods for
TITLE OF INVENTION: No. 6355466el motor proteins and methods for
TITLE OF INVENTION: Heir use
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
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590 RFNHPEEARA-ERQEQSLLR--HSVINSQLGSP--APGRHDRILSKA-
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39.2%; Pred. No. 7.8e-46;
iive 62; Mismatches 134;
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                                                                                              -GSDADGDSRSDSPLP-------
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Sequence 6, Application US/09572191
Patent No. 6355466
PAPPLICANT: Beraud, Christophe
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Best Local Similarity 39.29
Matches 167; Conservative
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ORGANISM: Human
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681 IKDLREEVKSKYGEGLNGLSAAARISEEVIGEFTQLHSQLHTSFNNLGKDLKSIFETMA 740
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741 THLSEOKNEINRLRAELQSSNRQNIETTHKASAHLAQAIEEEHVAAEAEREILMSQIKAL 800
                                                                                                                                                                                                                                                      699 VEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDA 758
                                                                                                                                                                                                                                                                                             801 VEESR----QKQF-ARLRAKIDGVRTEISASGDMLEQATTQHDRQIDEWVF---KSEQFA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 RSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSM---MGYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIKVVCRFRPLNDSEERAGSKFVVKF-----PNNVEENC-----ISIAGKVYLFD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFD 65
                                                                                     -----RTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQK-----I
                                                                                                                                                                     SHLTD--DELDALFDDVQK-----RGL
                                           627 TSVK-----VNEFIATEISNIERTRSDLSEYNRSLDAACNNAKAETSSAHEDMNNVLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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  573 TRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.5%; Score 625; DB 2; Length 41: 39.4%; Pred. No. 1.6e-44; Live 67; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P. STREET: 9035 South 700 East, Suite 200 CITY: Sandy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                               :| : : : : : : : : : | 853 KDVNASKDEIRTKLQNDWEAFDQRNSTIRKATESVHKE 890
                                                                                                                                                                                                                                                                                                                                       759 SNV------DVEELRQQQAQMEEALKTAKQE 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08713815A
Patent No. 5830659
GENERAL INFORMATION:
APPLICANT: RUSSell J. Stewart
TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
TITLE OF INVENTION: SEPARATIONS BY KINESINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T3214/U-2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: AST Ascentia 900N
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WORD Perfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,815A
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. HOWATCH
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T3214
TELECOMMUNICATION INFORMATION:
TELEFRAX: (801)566-6730
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 154; Conservative
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-713-815A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-713-815A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKV-----REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLRYADSAKRIKNHAVVNED-PNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGFVE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESYPPDTPLE----KQIVSIQQPDATVKKMSKA---EIVEQLNQSEKLYRDLNQTWEEKLA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| ::| ::| ::| ::| | ::| | ESY-EEMKMENESRRIISEEQ-RAKIESMESSLRHKVQELLTLTSK-FNDLKKDNDDTLA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ASGQTP 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGRVIAALADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KTEBIHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQ 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRVGNVNQ-----DTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKP 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%; Score 633; DB 4; Length 1184;
illarity 26.7%; Pred. No. 1.8e-44;
Conservative 161; Mismatches 315; Indels 168; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTI--MDGPKAFA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||: :| :| :| :| :| :| :| | | :||| :|||| :|||| :|||| :|||| :|||| :|||| :|||| :|||| :||||| :||||| DTLGILSDNAGIIPRVLYSLFAKLADTES-----TVKCSFIELYNEELRDLLSAEENPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFTLTLTQKWHDEETKMDTEKV - - AKISLVDLAGSERATSTGATGARLKEGAEINRSLST
| :| || || || || || || || || 354 LNFAQRAKLIKNKAVVNEDTQGNVSQLQAEVKRLKEQLAEL.
                                                                                                                                                                                                                                                                 APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TILE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                        Sequence 2, Application US/09541782
Patent No. 6284480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: A. nidulans
US-09-541-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                               404 PVEESY 409
                                                                                                    401 РЕЕННИ 406
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Best Local 9
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123 KEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREHP 182
    110 VKQGIIPRIVNDIFNHIYAM--EVNLEFHIKVSYYEIYMDKIRDLLDVS-KVNLSVHEDK 166
                                                                  g
                                                                oy
Dp
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Search completed: July 25, 2002, 05:45:05 Job time: 3939 sec

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2002, 05:38:41 ; Search time 44.64 Seconds (without alignments) 1687.590 Million cell updates/sec

Title: Perfect score: Sequence: US-09-235-416-1

MSGGGNIKVVVRVRPFNARE.....ELRQQQAQMEEALKTAKQEF 784

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database : PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	507 s	689.5	691.5	701	708	722	743	744	746.5	755.5	765.5	772	775	782.5	800	814	825.5	828.5	844.5	860	1034	1035	1147	1284.5	•	1590.5	1593.5	1663.5	1674	acore	
	17 1	17 1	17.2	17.4	17.6	17.9	18.4	18.5	18.5	18.7	19.0	19.2	•	•	19.9	20.2	20.5	20.6	21.0	21.3	25.7	25.7	28.5	31.9		39.5	39.5	41.3	41.5	March	Query
	1021	294	963	1130	672	929	935	1226	784	1225	793	928	1229	1231	701	955	786	742	747	699	1121	1121	928	1576	1921	1584	1584	1695	1150	rengen	
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2007	20712	538983	A41919	T21134	S54351	T51932	T51930	151617	A55236	A56514	JC5831	T10164	T48959	A54803	B44259	A47334	A53939	S58691	A57107	S38982	T13796	T13750	T16759	T29237	T13827	T15822	JN0114	A56921	A55289	1	;
vincath heavy chai	אַנוועטבוו דעדמעעם ער			hypothetical prote	kinesin osm-3 - Ca		kinesin [imported]	0		chromokinesin - ch	kinesin-related pr	kinesin heavy chai	kinesin-like prote	microtubule-associ	kinesin-related pr	inesin-re	kinesin homolog KH				_				kinesin-73 - fruit	kinesin-like prote	-related	kinesin family pro	ke pro	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	3 <u>1</u>	30
635.5	636.5	649.5	661.5	662.5	663	665	668	671.5	671.5	677	678	681	684	684.5	687
15.8	15.8	16.1	16.4	16.4	16.5	16.5	16.6	16.7	16.7	16.8	16.8	16.9	17.0	17.0	17.0
1083	1076	975	1388	2954	332	670	2663	1056	843	1027	1075	968	967	1032	881
2	N	ب	N	N	N	2	ب	-	N	N	N	N	۲	N	N
T26844	B84687	A31497	T30335	T14156	C48835	T29898	S28261	G02157	S44868	S37711	T45570	T51933	A35075	<b>I38510</b>	184737
hypothetical prote	probable kinesin-l	kinesin heavy chai	KLP2 protein - Afr	kinesin-related pr	kinesin-like prote	kinesin protein OS	centromere protein	kinesin-like spind	kinesin heavy chai	kinesin heavy chai	kinesin-like prote	kinesin motor prot	kinesin heavy chai	neuronal kinesin h	kinesin heavy chai

# ALIGNMENTS

A.32.03

Kinesin-like protein KIF1B - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Jan-2001
C;Accession: A55289
R;Nangaku, M; Sato-Yoshitake, R; Okada, Y; Noda, Y; Takemura, R; Yamazaki, H; H
Cell 79, 1209-1220, 1994
A;Title: KIF1B, a novel microtubule plus end-directed monomeric motor protein for tra
A;Reference number: A55289; MUID:95094296
A;Accession: A55289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1150 <NAN>
A;Cross-references: GB:D17577; NID:9407338; PIDN:BAA04503.1; PID:9407339
C;Superfamily: kinesin-related protein KIF1B; kinesin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;6-354/Domain: kinesin motor domain homology <KMOT>
F;97-104/Region: nucleotide-binding motif A (P-loop)

Que	Query Match 41.5%; Score 1674; DB 1; Length 1150;	
Mat	Hest Local similarity 43.4%; Fred. No. 1.2e-82; Matches 380; Conservative 137; Mismatches 237; Indels 122; Gaps 19;	
Qy	4 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPPGAEEKARKSGKTIMDGPKAFA 63	
Db	3 GASVKVAVRVRPENSRETSKESKCIIQMQGNSTSIINPKNPKEAPKSFS 51	
Qy	64 FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122	
Db	52 FDYSYWSHTSPEDPCFASQURVYNDIGKEMILHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111	
Qy	123 KEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180	
Db	112 EESQAVIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE 170	
Qy	181 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240	
DЬ	171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKQ 230	
Qy	241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300	
В	231 DPETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVSK 290	
Qy	301 GKOKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIK 360	
뮹	291 -KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIK 349	
Qy	361 NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGVEESYPPDTPLEKQ 418	
망	350 CNAVINEDPNAKLYRELKEEVTRIKDLLRAQGIGDIIDTSMGSLTSSPSSCSLNSQVG 407	

```
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Mesidues: 1-1695 <RES> A;Cross-references: GB:D29951; NID:g976234; PIDN:BAA0622 A;Cross-references: GB:D29951; NID:g976234; PIDN:BAA0622 C;Superfamily: kinesin-related protein unc-104; kinesin C;Keywords: nucleotide binding; P-loop F;6-360/Domain: kinesin motor domain homology <KMOT> F;97-104/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
A56921
A56921
A56921
Klnesin family protein KIFla - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C; Accession: A56921
R; Okada, Y: Yamazaki, H: Sekine-Alzawa, Y: Hirokawa, N.
Cell 81, 769-780, 1995
A; Title: The neuron-specific kinesin superfamily protein KIFlA i.
A; Reference number: A56921; MUID:95292344
A; Accession: A56921
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Best Local Similarity
Matches 350; Conserv
                    179
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REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK
                                                                    YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV
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                                                                                                                      EDRSYMSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                                                                                                                            GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS
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                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                41.3%; Score 1663.5; DB 2;
46.5%; Pred. No. 7.8e-82;
tive 126; Mismatches 167;
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SVKVAVRVRPFNQREISNTSKCVLQVNGNTTTI------

NGHSINKENESENED

50

123

Gaps

19;

prot

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NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFD

Conservative

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C:Superfamily: kinesin-related protein unc-104; kinesin motor domain homology; C:Keywords: ATP; microtubule binding; nucleotide binding; P-loop F:4-353/Domain: kinesin motor domain homology <KMOT>
F:93-100/Region: nucleotide-binding motif A (P-loop)
F:1285-1287/Region: cell attachment (R-G-D) motif F:99/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinesin-related protein unc-104 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
JN0114
                                                                                                                                                                                                                          C; Genetics:
A; Gene: unc-104
                                                                                                                                                                                                                                                               A;Cross-references: GB:M58582
A;Note: 598-Thr and 930-Met were also
                                                                                                                                                                                                                                                                                                                                              A;Title: The C. elegans unc-104 gene encodes a putative kinesin heavy chain-like A;Reference number: JN0114; MUID:91097805
A;Accession: JN0114
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Neuron 6, 113-122, 1991
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A; Residues: 1-1584 <OTS>
    Query Match
Best Local S
Matches 356
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      Local Similarity
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39.5%; Score 1593.5; DB 1; 44.7%; Pred. No. 4.3e-78; tive 139; Mismatches 213;
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                                                                                                                                                                                                                                                                 found
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                                       1584;
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RESULT 4
T15822
Kinesin-like protein unc-104 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
C;Accession: T15822
R;Du, Z.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C52E12.
A;Reference number: Z18412
A;Accession: T15822
A;Accession: T15822
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1584 <DUZ>
A;Cross-references: EMBL:U50135; NID:g1208884; PID:g1208885; PIDN:AAA93453.1; C:Genetics:
A;Gene: CESP:unc-104
A;Introns: 34/1; 84/2; 140/3; 200/2; 285/3; 339/2; 490/2; 580/1; 631/3; 672/1; :C;Superfamily: kinesin-related protein unc-104; kinesin motor domain homology; i
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                         200/2; 285/3; 339/2; 490/2; 580/1; 631/3; 672/1; d protein unc-104; kinesin motor domain homology;
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           R:Li, H.P.; Liu, Z.M.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 94, 1086-1091, A;Title: Kinesin-73 in the nervous system of A;Reference number: Z17784; MUID:97188425 A;Accession: T13827
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RESULT 5
T13827
Kinesin-73 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-19-
C;Accession: T13827
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                                                                                                                                                  VE--LKKKVQFQFALLT
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translated from GB/EMBL/DDBJ

Drosophila

embryos

#text\_change 17-Nov-2000

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hypothetical protein F56E3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Fe
C;Accession: T29237
R;Gattung, S; Wu, X.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F56E3.
A;Reference number: Z20592
A;Accession: T29237
A;Accession: T29237
A;Molecule type: DNA
A;Residues: 1-1576 <GAT>
A;Residues: 1-1576 <GAT>
A;Cross-references: EMBL:U41536; PIDN:AAB52613.1; GSPDB:GN00028; CESI
A;Experimental source: strain Bristol N2; clone F56E3
C;Genetics:
                                                                                                                                                                                                                         RESULT
T29237
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A; Residues: 1-1921 <LTH>
A; Cross-references: EMBL:U81788; NID:g1906595;
C; Genetics:
A; Cross-references: FlyBase:FBgn0019968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-QLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKNHAV
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                                                                                                                                                                                                                                                                                EPQTPAQLIDYNFARDEIMQNELSN
                                                                                                                                                                                                                                                                                                                                      ITIEDSGLYMEPVQGARCFVNGSAAVEKTPLQNGDRILWGNHHFFRVNSPKSNNTSMCAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNEDPNARI IRELRHEVETLRSMLKHA-----TGSPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQKK 305
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                                                                                                                                                                                                                                                                                                                                                                                             -GIKVEKNKYYLVNLNADPSLNELLVYYLKDRTLIGGRTISGQQPDIQLSGLGIQPEHCV
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Pred. No. 2.5e-67;
B; Mismatches 171;
                                                                                                                                                                                                                                                                                                           618
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                                 CESP:F56E3
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A;Map position: X
A;Introns: 23/1; 47/2;
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Best Local Sin
Matches 323;
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                                                                                                  AV---DQYMESVT----
                                                                                                                  AILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDS--QSSFPVRDKYMSNGT
                                                                                                                                                   SIMEDSTMFDY -------NDAWHEVNDANPI---
                                                                                                                                                                                                  YGGRLRLFVAPMSSECRICVNGKQITERTLLRNGNRLLVGMNHFFKVNCP---KVMDMEQ
                                                                                                                                                                                                                                                                               NIKPGQTRVGN-----VNQDT------
                                                                                                                                                                                                                                                                                                                     NQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVY
                                                                                                                                                                                                                                                                                                                                                                       GGGGGGAGGSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDL
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RLKAD
                                                 AGGETPSTPMT-PGECLPTPITTPTGLPPFPFPANPKQSVKSKFFYWAQRKEEMFAESLK
                                                                         IDNFSLDTATTMPG----TPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQMEEALK
                                                                                                                                                                          SLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAAS
                                                                                                                                                                                                               VDNVVT--IVP-NEKAAVMVNGVRIDKPTRLRSGYRIIIGDEHIFRENHPEEARAERQEQ 604
                                                                                                                                                                                                                                                     YIN-GSAIIGNSEELETSRDSGLSMTCSDSSRRDDDKERTSIVLRGLGIMRRHAKMTVEE
                                                                                                                                                                                                                                                                                                       NKSWEERLKETDTLNKERQKDLTEIGISIESS--GIKVEKDRFYLVNMNADPSLNELLVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYVFINQKLDFRSLTTLGMVISALAERNS---KKDKFIPYRDSVLTWLLKDSLGGNSRTV
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23; Conservative
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Pred. No. 2.1e-61;
0; Mismatches 217;
                                                                                                                                                                                                                                                                              -----QAEIRLNGSKILKEHC--TFEN
                                                                                                  LKHQEDKKAALEQQYEAFEKYIQSLT
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RESULT T16759

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R; Ravello, T. he EMBL Data Library, March 1995 submitted to the EMBL Data Library, March 1995 A; Description: The sequence of C. elegans cosmid R14 A; Reference number: 218571 A; Accession: T16759 A; Accession: T16759 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 80/3; 125/1; 261/2; 331/3; 350/2; 516/3; 589/1; 615/2; 638/3;
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A; Residues: 1-928 <FAV>
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Best Local S
Matches 281
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                                                                                                                                                                                                                                                                                                       SYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHK
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GLTE
                        GLVE 700
                                                                                                            NHLYVENNPTKKG-
                                                                                                                                                               GNFIQMSGLSILPQHVTLKNDGNNQIHLSPCSEDLDIFINGKPVHGETQLQQNDRVFFGG
                                                                                                                                                                                         QAEIRLNGSKILKEHCTFEN-VDNVVTIVP-NEKAAVMVNGVRIDKPTRLRSGYRIILGD
                                                                                                                                                                                                                        HASGASEKVEMEAKK---
                                                                                                                                                                                                                                                                           STLRFADRAKSIKTNAVVNENQTERALRELREENLRLQSQIQ-----GGTAG-----
                                                                                                                                                                                                                                                                                                                                                 STLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGFVEE
                                                                                                                                                                                                                                                                                                                                                                                                           LGRVIAALADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETL
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                                                                               ----SPLPHFRGKDSDWFYARREAASAILGLDQKIS-HLTDDELDALFDDVQKARAVRR
                                                                                                                                   FHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSD---
                                                                                                                                                                                                                                                                                                                                                                                          LGRVIKALHDSQKAKSGKKTQIPYRDSVLTCLLKNALGGNSKTIMIAAISPADINFEETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%; Score 1147; DB 2; illarity 38.8%; Pred. No. 2.7e-54; Conservative 116; Mismatches 217;
                                                                                                         ----IRTDITYENAQAEIAQNHAAALGNRG--LGGGSKRDLIL
                                                    LVQRANAMATELGRNVKFEIVLVSPEM-
                                                                                                                                                                                                                       -KKMCHLWNLNEDPALTNVIVHFIPVGESVVGNKPTSS
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R;Ohkura, H.; Torok, T.; Tick, G.; Hoheisel, J.; Kiss, I.; Glover, D.M. J. Cell Sci. 110, 945-954, 1997
A;Title: Mutation of a gene for a Drosophila kinesin like protein, KLP38B, A;Reference number: Z17752; MUID:97296456
A;Accession: T13750
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13750
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A;Cross-references:
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A;Molecule type: mRNA
A;Residues: 1-1121 COHK>
A;Cross-references: EMBL:Y10667; NID:g2253151; PIDN
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                                                                                FENV--DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP---EEARA
                                                                                                                                                                                                                                                               PYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKNHAVVNEDP
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                                                  IEHERGGKLYVIPGSEDFETYVNGELLKDRRQLFHGDRLVIGGSHYFRISNPFCSQRGKA
                                                                                                                         EQKQACLVNLTADPILSGTLFYLLPQGLVRIGRGRLPGGSSSSQPDIVLDGPLVALQHCS
                                                                                                                                                       SKEMPHLVNLSDDPLLAECLVYNIKPGQTRVG-----NVNQDTQAEIRLNGSKILKEHCT
                                                                                                                                                                                             LRQQLAERERELSRAQK-----SWMEKLKEAEDQRKSELRVLKRRGLALEL----TA
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RESULT 9
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kinesin-related protein 38B - fruit fly (Drosophila melanogaster) (fra
C:Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov
C;Accession: T13796
R;Molina, I.; Baars, S.; Hales, K.; Fuller, M.T.; Ripoll, P.
J. Cell Biol. 139, 1361-1371, 1997
A;Title: A chromatin associated kinesin-related protein requiered for
A;Reference number: Z17759; MUID:98060833
A;Accession: T13796
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBD:Y15247; NID:g2578010; PIDN:CAA75531.1; PID:g2
C:Genetics:
L:Genetics:
A;Cross-references: EMBD:Y15247; NID:g2578010; PIDN:CAA75531.1; PID:g2
C:Genetics:
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A;Cross-references: FlyBase:FBgn0004374
C;Superfamily: kinesin-related protein Eg5; kinesin motor domain
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      HLVNLSDDPLLAECLVYNIKPGQTRVG---
                                                                                            AEIVEQLIQSEKLYRDLIQTWEEKLAKTEEIHKEREAALEELGISIEKGFVGPYHSKEMP
                                                                                                                                      RDLRAEYDRLKSLRNEYERQRRLSGNSNNPYPRKIIIET-----SVDETEVEALRQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274;
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                                              -SWMEKLKEAEDQRKSELRVLKRRGLALEL----TAEQKQA 634
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Pred. No. 4.6e-48;
0; Mismatches 290;
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      -- NVNQDTQAEIRLNGSKILKEHCTFENV-
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A;Title: Novel heterotrimeric kinesin-related protein purified from sea urch A;Reference number: S38982; MUID:94050179
A;Accession: S38982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Molecule type: protein
A; Residues: 2-5, 'X', 7-11;59-64;125-132;222-226, 'X', 228-230 <COL2>
A; Residues: 2-5, 'X', 7-11;59-64;125-132;222-226, 'X', 228-230 <COL2>
C; Complex: heterotrimer of a 115K chain and two kinesin related chains of 95K (PIR:S5 C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology (C; Keywords: ATP; heterotrimer; microtuble binding; nucleotide binding; P-loop F;11-348/Domain: kinesin motor domain homology <KNOT>
F;17-104/Region: nucleotide-binding motif A (P-loop)
F;103/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-699 <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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Matches 205;
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                                                                                                                                                                                                                                                                                             YGKE---HGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLK 177
                                                                                                                                                                                                                                                                                                                                                                                                   AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGGNIKVVVRVRPFNAREIDRGAKCIVRM-EGNQTILTPPPGAEEKARKSGKTIMDGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWFYARREAASAILGLDQKISHLTDDELDALFDDVQKA---RAVRRGLVEDNEDSDSQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVD---
                                            LADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD
                                                                                        ----SDMGLDKEQHVRVGKLHMVDLAGSERQTKTGATGQRLKEATKINLSLSTLGNVISS
                                                                                                               VKERPDVGVYVKDLSAFVVNNADDMDRIMTLGNKNRSVGATNMNESSSRSHAIFTITLER
                                                                                                                                                                                                  VREHPSTGPTVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQ
                                                                                                                                                                                                                                                                      VRSQPELRGIIPNSFAHIFGHI--AKEQENVRFLVRVSYLEIYNEEVKDLLGKDQQHRLE
                                                                                                                                                                                                                                                                                                                                                              SFTFDTVF-----APG-AKQTDVYNQTARPIVDAIIEGYNGTIFAYGQTGTGKTFTMEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNDNVRVVVRCRPLNSKETGQGFKSVVKMDEMRGTVQVTNPNA-----PSG----EPPK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPVRD------KYMSNGTIDNFSL 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMLETERQA----LALAQQQEHTPLRHEDAVSTPAQKSTILEDIQRIMLNPSEESLHKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQLAHQEILQKQEQQLRSELEAEKRAALTKIEQERAQHARDFEERLQCLELEQFKYKCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLLRH----SVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDS-----PLPHFRGK-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGKLYVIPGSEDFETYVNGELLKDRRQLFHGDRLVIGGSHYFRISNPFCSQRGKADHPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP---EEARAERQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
-GKSTHIPYRNSKLTRLLQDSLGGNAKTVMCANIGPAEYNYDETISTLRYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:L16993; NID:g295245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 860; DB 1;
Pred. No. 5.9e-39;
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gg Qy	В <b>2</b> 9	Ωу	Db Qq	Db Qq	Query Best I Matche	A; Res C; Con C; Sup F; 9-	A; Acc A; Sta A; Mol	R; Ras	C; Spe	RESUI S5869 kines	Db Qy	Db !	O <sub>V</sub>	Db Oy	Db	Qy	Db Qy	Db	Qy	뮍
241 224	181 168	124 111	59	9	ery Ma st Loa ches	nplex perfar words 45/Do 102/I	cerencession	hid, bl. B.	erna cies	1	660	601	618	572 541	503	512	460 448	396	405	336
DEETKHDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALAD 297	HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNNNETSSRSHAVFTLTLTQKWH 240           :  :         :  :        :  :	EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180      : :	DRSY-WSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGK 123        :	IKVVVRVRPFNAREIDRGAKCIVRMEGNOTILTPPPGAEEKARKSGKTIMDGPKAFAF 64 :           ::   :          : : :        :	Match 20.6%; Score 828.5; DB 1; Length 742; Local Similarity 31.5%; Pred. No. 3.3e-37; Les 250; Conservative 122; Mismatches 286; Indels 135; Gaps 25;	A; Residues: 1-742 < CASS> C; Complex: heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR:S3 C; Complex: heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR:S3 C; Superfamily: kinesin-related protein KIF3; kinesin motor domain homology C; Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop E; 9-345/Domain: kinesin motor domain homology < KMOT> F; 95-102/Region: nucleotide-binding motif A (P-loop) F; 101/Binding site: ATP (Lys) #status predicted	ce number: \$38691; MUID:95404610 sn: \$58691 preliminary; nucleic acid sequence not shown; not compared with conceptual type: mRNA	nn: 53691 D.J.; Wedaman, K.P.; Scholey, J.M. Iol. 252, 157-162, 1995 Heterodimerization of the two motor subunits of the heterotrimeric kinesin,	e names: kinesin-2 chain B; kkP (85/95) 95k chain :Strongylocentrotus droebechiensis )-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001	2 - sea urchin (Strongylocentrotus droebechiensis)	DWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSF 711	RSFFDDEEDHWKLHPITRLENQQMMKRPVSAVGYKRPLSQHARMSMMIRPEPRYRAEN- 65		PTRLRSGYRIIIGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLG 617	KRREREIQQQMESRDEETLELKETYTSLQQEVDIKTKK 540	NIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDK 571	AKTEEIHKEREAALEELGISIEKGEVGPYHSKEMPHLVNLSDDPLLAECLVY 511	EEEEGEEGEEDGDDKDDYWREQQEKLEIEKRAIVEDHSLVAEEKMRLLKEKE 447	LNQTWEEKL : :	RAKNIKNKPRVNEDPKDALLREFQEEIARLKAQLEKRSIGRRKRREKRREGGGSGGGEE 395

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C;Species: Chlamydomonas reinhardtii
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001
C;Accession: A53939
R;Walther, Z: Vashishtha, M.; Hall, J.L.
J. Cell Biol. 126, 175-188, 1994
A;Title: The Chlamydomonas FLA10 gene encodes a novel kinesin-homologous prote:
A;Reference number: A53939
A;Accession: A53939
A;Accession: A53939
A;Accession: A53939
A;Cross-references: EMBL: L3697; NID:94299638
A;Residues: 1-786 <WALD
A;Residues: 1-786 <WALD
A;Cross-references: EMBL: L3697; NID:9497696; PIDN:AAA21738.1; PID:9497697
A;Note: authors translated the codon AAC for residue 753 as Asp
C;Genetics:
A;Gene: FLA10
C;Keywords: ATP; coiled coil; nucleotide binding; P-loop
F;11-359/Domain: kinesin motor domain homology <KMOT>
F;97-104/Region: nucleotide-binding motif A (P-loop)
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C;Species: Chlamydomonas reinhardtii
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994
C;Accession: A53939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RERDMERKLKEQDDKTVEIEGTFSSLQQEVE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEREAALEELGISIEKGFVGPY----HSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEEEGDEMDEEEMYKESQQKLEE---EKEKIMANQSMIAEEKQKLLSEVQKRQGEIKKEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLT--DDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFPV-----RDKYMSNGTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLLTPLAKAEGPSQMAKRPVSAVGNRRPIAD--YARMAAQMGGNPRYKAENILSVDLDMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSDIQDLQDEHARERQELEQTQNELIRELKLKKVIADNFIPVEERTKITTRAVFDEETEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQKEMLEGKIKAMESKLLVGGKSIVDHTNEQQRKIE-EQRLLLAE-----EKN 501
                                                                                                 SGGG--NIKVVVRVPFNAREIDRGAKCIVRME---GNQTILTPPPFGAEEKARKSGKTIM 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NXTTRDYEGPSVAPRVQ----AALDAALQDEDDLDLEVQPEVFKAKTKLKKDKVRSK----
                                       DGPKAFAFDRSY-WSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKS 115
                                                                               AGGGSESVKVVVRCRPLNGKEKADGRSRIVDMDVDAGQVKVRNPKADASEP------
  --PKAFTFDQVYDWN
                                                                                                                                                              Conservative
                                                                                                                                                                              20.5%; Score 825.5; DB 2; 39.3%; Pred. No. 5.1e-37;
                                                                                                                                                              80; Mismatches 168;
-CQQRDVFDITARPLIDSCIEGYNGTIFAYGQTGTGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel kinesin-homologous protein.
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                                                                                                                                                                                                 Length
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    104
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C;Accession: A47334
C;Accession: A47334
R;Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghalib, H.W.; Badaro, R.; Reed, S.G. Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993
A;Title: Molecular characterization of a kinesin-related antigen of Leishmania chagas A;Reference number: A47334; MUID:93133867
A;Recession: A47334
A;Recession: A47334; MUID:93133867
A;Recession: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-955 <BUR>
A;Residues: 1-955 <BUR>
A;Residues: 1-955 <BUR>
A;Rote: sequence: GB:LO7879; NID:9308884; PIDN:AAA29254.1; PID:9308885
A;Cross-references: GB:LO7879; NID:9308884; PIDN:AAA29254.1; PID:9308885
A;Cross-references: GB:LO7879; NID:9308884; PIDN:AAA29254.1; PID:9308885
C;Superimental source: MHOM/BR/82/BA-2,Cl
A;Rote: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
C;Keywords: ATP; nuclectide binding; P-loop
F;13-398/Domain: kinesin motor domain homology <KMOT>
F;122-129/Region: nuclectide-binding motif A (P-loop)
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C;Species: Leishmania chagasi
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
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GKRKKGYKGGGEEYYVDVREHPSRGYFLEGQRLVEYGSLDDVVRLIEIGNGVRHTASTKM
                                           NPSTKG-----NLKVREHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNM
                                                                                                                    SYSMMG-----YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLL 168
                                                                                                                                                                                 ----FQEDHVEWSVETPDACGATPATQADVERTIGYPLVQHAFDGENSCLFAYGQTGSGK 128
                                                                                                                                                                                                                               GPKAFAFDRSYWSF---DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGK 114
                                                                                                                                                                                                                                                                              VKVSVRVRPLNERENNAPEGTKVTVAAKQAAAVVTVKVLGGSNNSGAAESMGTARRVAQD
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                                                                                          TYTMMGADVSALSGEGNGVTPRICLEIFARKASVEAQGHSRWIVELGYVEVYNERVSDLL
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                          20.2%; Score 814; DB 2;
28.1%; Pred. No. 2.8e-36;
tive 125; Mismatches 292
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Query Match Best Local Similarity

19.9%;

Score 800; DB 1 Pred. No. 1e-35;

DB 1; Length

25;

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RESULT 15
B44259
kinesin-related protein KIF3A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994
C;Accession: B44259; S27872
R;Aizawa, H:; Sekine, Y:; Takemura, R:; Zhang, Z.;
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous
A: Peference number: A44259; MUID:93077686
             A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal trec;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology C;Keywords: ATP; coiled coil; heterodiner; heterotrimer; microtubule binding; nucleotide F;1-368/Domain: head globular #status predicted <HGL>F;15-351/Domain: kinesin motor domain homology <KWOT>F;150-107/Region: nucleotide-binding motif A (P-10op) F;369-599/Domain: helical rod #status predicted <ROD>F;369-599/Domain: helical rod #status predicted <ROD>F;600-701/Domain: tail globular #status predicted <TGL>F:100-107/Johnain: tail globular #status predicted <TGL>F:100-107/Johnain
                                                                                                                                                                                                                                       A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:118911)
C; Complex: heterodimer with KIF3B (PIR:A57107); the KIF3A/3B
C; Function:
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GRRKRS
                              GRHDRT
                                                         NMMRKQTPVPDKKERDPFEVDLS--HVY-LAYTEESL--RQSLMKLERPRTSKGKARPKT
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                                                                                                                      HQREIEGLLENIRQLSRELRLQMLIIDNFIPQDYQEMIENYVHWNEDIGEWQLKCVAYTG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

SwissProt\_40:\*

### SUMMARIES

Result

DB ID  KF1C_HUMAN  KF1A_HUMAN  KF1B_HOUSE  KF1B_HOUSE  KF1B_RAT  KF1B_AT  KF1B_AT  KF1B_AT  KF1B_HUMAN  KF1B_HUMAN  KF1B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF3B_HOUSE  KF4A_HUMAN  KF4A_HUMAN  KF4A_HUMAN  KF4A_CHICK  KF3C_RAT  KF3C_RAT  KF3C_RAT  KF3C_RAT  KF4A_CHICK  KF3C_RAT  KF4A_CHICK  KF3C_RAT  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KF4A_CHICK  KK1ML_WGUSE  KF4A_CHICK  KK1ML_WGUSE  KF3C_RAT  KK1ML_WGUSE  KF3C_RAT  KK1ML_GUSE  KF4A_CHICK  KK1A_CHICK  KK1ML_GUSE  KK1ML_GUSE

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EG51_XENLA	KIP1_YEAST	EG52_XENLA	KLP5_SCHPO	BIMC_EMENI	K125_ARATH	KINH_DROME	CENE_HUMAN	KF5C_MOUSE	KF5C_HUMAN	KINH_CAEEL	EG5_HUMAN
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xenopus	saccharo	xenopus ]	schizosac	emericel]	arabidopsis	drosoph11	homo sapi	mus muscu	homo sapi	caenorhab	homo sapi

# ALIGNMENTS

######################################	RESULTA ACC OCC ME E E E E E E E E E E E E E E E E E
"Characterization of KIFIC, a new kinesin-like protein involved in vesicle transport from the Golgi apparatus to the endoplasmic reticulum.";  J. BLOI. Chem. 273:20267-20275(1998).  [2]  SEQUENCE FROM N.A.  "ITSSUE-Brain; MEDLIKE-98403880; PubMed-9734811; ISSIE-Brain; MEDLIKE-98403880; PubMed-9734811; The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; PROTECTED FOR THE RETROGRADE TRANSPORT OF GOLGI CODE FOR THE RETROGRADE TRANSPORT OF GOLGI CODE FOR THE RETROGRADE TRANSPORT OF GOLGI CODE FOR THE SETTIOLUM. HAS A MICROTUBULE PLUS END-PRICTED MOTILITY.  "ITSSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED, WITH MOST ABUNDANT EXPRESSION IN HEART AND SKELETAL MUSCLE.  "ITSSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED, WITH MOST ABUNDANT EXPRESSION IN HEART AND SKELETAL MUSCLE.  "ITSSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED, WITH MOST ABUNDANT EXPRESSION IN HEART AND SKELETAL MUSCLE.  "ITSSUE SPECIFICITY IS COPYIGHT. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ EMBL; U91329, AAC52117.1;  EMBL; MEDLIKE SALE AND SALE.  "EMBL; MEDLIKE SALE.  "EMBL; MEDLIKE SALE.  "EMBL; MEDLIKE SALE.  "EMBL; MEDLIKE SALE.  "EMBL;	UMAN  FIC_HUMAN  \$TANDARD; PRT; 1103 AA.  43996; 075186;  5-DEC-1998 (Rel. 37, Created)  5-DEC-1998 (Rel. 37, Last sequence update)  6-CCT-2001 (Rel. 40, Last annotation update)  inesin-like protein KIFIC.  IFIC OR KLAA0706.  ORD Sapiens (Human).  ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  CBI_TaxID-9606;  1]  EQUENCE FROM N.A.  ISSUE-Hippocampus;  ISSUE-Hippocampus;  EDLINE-98352063; PubMed-9685376;  Corner C., Ciossek T., Mueller S., Moeller N.P.H., Ullrich A., Characterization of KIEIC a new kinesin-like protein involved.

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           NGVRIDKPTRLRSGYRIILGDFHIFRENHPEEARAERQEQSLLRHSVTNSQLGSPAPGRH
                                                      VYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENV-----DNVVTIVPNEKAAVMV
                                                                                               NQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECL
                                                                                                                               PVSPSSPTTHNGELEPSFSPNT--ESQI------GPEEAMERLQETEKIIAEL
                                                                                                                                                                         CNAIINEDPNARLIRELQEEVARLRELLMAQGLSASALEGLKTEEGSVRGALPAVSSPPA
                                                                                                                                                                                     HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                                                                                                                                                                                                                                                                                     FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                   GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                                                                                                                                                                                                            HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH
                                                                                                                                                                                                                                                                                                                                                 EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE
                                                                                                                                                                                                                                                                                                                                                                                         FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ
 NGKLVTEPLVLKSGNRIVMGKNHVFRFNHPEQARLERER--
                                          LYHIKDGVTRVGQVDMD----IKLTGQFIREQHCLFRSIPQPDGEVVVTLEPCEGAETYV
                                                                                    NETWEEKLRKTEALRMEREALLAEMGVAVREDGGTVGVFSPKKTPHLVNLNEDPLMSECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000253;
IPR001752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.48;
nilarity 47.58;
Conservative 12:
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438
523
633
828
97
669
955
                                                                                                                                                   SGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINESIN-MOTOR (BY SIMILARITY).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
FHA.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1667; DB 1;
Pred. No. 1.7e-81;
1; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
Q -> R (IN REF. 2).
LMGPGRGV -> SGGRGGGL (IN REF. NV -> KL (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F14BC398D4B2EC10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
-GVPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114;
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 RESULT 2
KF1A_HUMAN
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Q12756;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1998
Q1-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIFIA OR ATSv.
Homo sapiens (Human).
-- "arvota; Metazoa; Chordata; "heria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Furlong R.A., Zhou C.Y., Ferguson-Smith M.A., Affara N.A., "Characterization of a kinesin-related gene ATSV, within the sclerosis locus (TSC1) candidate region on chromosome 9934 Genomics 33:421-429(1996).

-I- FUNCTION: MOTOR FOR ANTEROGRADE AXONAL TRANSPORT OF SY
                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
NP_BIND
SEQUENCE
                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                 EMBL; X90840; CAA62
HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinesin-like
                         DOMAIN
DOMAIN
                                                                                                                                PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; PROSITE; PS50006; FHA_DOMAIN; 1.

PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                             PRINTS; PR00380; KINESINHEAVY. SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                     Pfam; PF00498; FHA; 1.
                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                          MIM; 601255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                InterPro; IPR001849; InterPro; IPR001752;
                                                                                                                                                                                                                                                                                                           InterPro; IPR000253;
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SIMILARITY: CONTAINS 1 FHA DOMAI
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SM00233; PH; 1.
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366
429
516
622
801
1575
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
e protein KIFIA (Axonal transporter
                    n; Microtubules; ATP-binding; Co.
1 361 KINESIN-MOTOR,
366 383 COILED COIL (PO)
429 462 COILED COIL (PO)
516 572 FHA.
522 681 COILED COIL (PO)
801 822 COILED COIL (PO)
901 822 PH.
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             ATP
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 (POTENTIAL).
D8DDEC784624FB4D CRC64;
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                                                                            (POTENTIAL).
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                                     (POTENTIAL).
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as its content
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Best Local
FIA, MOUSE STANDARD; P
933173; 061770;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequ
15-JUL-1998 (Rel. 36, Last anno
Kinesin-like protein KIFIA.
KIFIA OR KIFI
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Rodentia; S:
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                        689
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                                                                                                                                                                                                 QKARAVRRGLVEDNEDSDSQSSFPVRDKYMSN 720
                                                                                                                                                                                                                                                                                                                                                                EEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNI
|||| :|| | |||| ||:|:: | :| :|| ||||||:|||:|||:||
EEKLRTTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLVNLNEDPLASECLLYYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                                                                                                                  RREREEATYLLE-QQRLDYESKLEALQKQMDS
                                                                                                                                                                                                                                                  SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV
                                                                                                                                                                                                                                                                         VTEPSILRSGNRIIMGKSHVFRFTHPEQARQERER---
                                                                                                                                                                                                                                                                                     IDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTL
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                                                                            . 27, Created)
. 35, Last sequ
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                                                                               Last sequence up
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Pred. No. 4.7e-81;
                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                             1695
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GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA

Query Match Best Local S Matches 350

Similarity

41.3%;

Conservative

126;

Score 1663.5; I Pred. No. 4.8e-1 26; Mismatches :

DB 1;

Indels Length

109; 1695

Gaps 63

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STITITITITI REPRESENTATE DE LA REPRESENTATION DE LA
                                                                                                                                                                                                                                     PRINTS; PRO0380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
SMART; SM00123; PH; 1.
PROSITE; PS00411; KINESIN_MOTOR
PROSITE; PS50067; KINESIN_MOTOR
PROSITE; PS50066; FHA_DOMAIN; 1
MOTOR PRO
DOMAIN
DOMAIN
DOMAIN
DOMAIN
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursors.";
Cell 81:769-780(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Brain;
MEDLINE-95292344; PubMed=7539720;
MEDLINE-95292344; PubMed=7539720;
Okada Y., Yamazaki H., Sekine-Alzawa Y., Hirokawa N.;
"The neuron-specific kinesin superfamily protein KIFIA is a unique monomeric motor for anterograde axonal transport of synaptic vesicle
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000253; FHA_domain.
InterPro; IPR001849; PH.
InterPro; IPR001752; kinesin.
Pfam; PF00498; FHA; 1.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93077686; PubMed-1447303; Aizawa H., Sekine Y., Takemura R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D29951; BAA06221.1;
                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                           PF00169; PH; 1
                                                                                                                                                                                                                                     PS00411; KINESIN_MOTOR_DOMAIN1;
PS50067; KINESIN_MOTOR_DOMAIN2;
PS50006; FHA_DOMAIN; 1.
                      366
429
516
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                      361
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(BY SIMILARITY).
D6EC3B88CBC9CCC6 CRC64;
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KFILB. MOUSE STANDARD,
Q60575; Q9WVE5; Q9R0B4; Q9Z119;
Q1-NOV-1997 (Rel. 35, Created)
P. 16-OCT-2001 (Rel. 40, Last sequence updar
P. 16-OCT-2001 (Rel. 40, Last annotation up
R. Kinesin-like protein KIFIB.
                                                                                                                                                                                                                                         MOUSE
"KIF1B, a novel microtubule plus end-directed for transport of mitochondria."; cell 79:1209-1220(1994).
                                 MEDLINE-95094296; PubMed-7528108;
Nangaku M., Sato-Yoshitake R., Okada
Yamazaki H., Hirokawa N.;
                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                      TISSUE-Brain;
                                                                                SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10090
                                                                                                                                            Mus musculus (Mouse)
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                                                                                  (ISOFORM
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                                                                                                                     Rodentia;
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                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                              Noda
                                         Υ.,
                       monomeric motor protein
                                              Takemura
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                                                                      SMART; SM00129; KISC; 1.
SMART; SM00233; PH; 1.
PROSITE; PS00041; KINESIN_MOTOR_DOMAIN1;
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
PROSITE; PS50006; FHA_DOMAIN; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
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SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-ICR; TISSUE-Brain;
MEDLINE-20035818; PubMed-10571041;
Gong T.L., Winnicki R.S., Kohrman D.C., Lomax M.I.;
"A novel kinesin of the UNC-104/KIF1 subfamily encoded
                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene.";
Gene 239:117-127(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999)
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                DOMAIN
                             DOMAIN
                                          DOMAIN
                                                      Alternative
                                                                  Motor protein; Microtubules;
                                                                                                                                                                          PRINTS; PR00380; KINESINHEAVY
                                                                                                                                                                                                    Piam;
                                                                                                                                                                                                                           InterPro; IPR000253;
InterPro; IPR001849;
InterPro; IPR001752;
                                                                                                                                                                                                                                                                   HSSP; P33176; 1BG2.
MGD; MGI:108426; Kif1b.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The major brain isoform of kiflb lacks binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
- SIMILARITY:
- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER.

SUBCELLULAR LOCATION: PREDOMINANTLY FOUND ON THE TUBULE-LIKE STRUCTURES WITHIN THE CYTOPLASM.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY TISSUE (MAINLY IN THE CEREBELLUM AND CEREBRUM) WI TYPE OF NEURONAL CELL.

SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (FEB-1999) to the EMBL/GenBank/DDBJ FUNCTION: MOTOR FOR ANTEROGRADE TRANSPORT
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                                                                                                                                                                                                                                                                                           D17577; BAA04503.1; -. AF090190; AAF06718.1; -. AF131865; AAD39438.1; -. AB023656; BAA75243.1; -.
                                                                                                                                                                                     PF00225; kinesin; 1. PF00169; PH; 1.
                                                                                                                                                                                                               PF00498; FHA; 1
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SM00129; KISC; 1.
e splicing.
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365 386
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556 612
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on and characterization of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buckmaster E.A., Tarlton
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 KINESIN-MOTOR.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
FHA.
                                                                  ATP-binding; Coiled
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OF MITOCHONDRIA. HAS
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Matches 357; Conserv
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| || : ||||:||:||:||:||::|
| petnlstekvskislvdlagseradstgakgtrlkeganinkslttlgkvisalaevdn
                                                                                                                                                                 HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                                                                                 KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
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ESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
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AKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGGKYLK
                                                 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVETQKKQ
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SELFSDGHDEFYDSSWFILVCRAFYDDTGSDAGTEEG
SELFSDGHDEFYDSSWFILVCRAFYDLKYPYLIHRV
AIVSEKGEVRGFLRVAVQAIAADEAEDYDSGSIAOSGTAKI
SFDNEYENQSDFSSAAMTRSGLSLEELRIVEGQGOSSEVIS
PPEEVNRAMDLDLKSGTLLDGKRVMEGFSSEIGNHLKLGSA
FTFRYTVLQASGILPEYADIFCQFNFLERHDEAFSTEPLKN
NGRGSPLGFYHVQNIAVEVTESFVDYIKTRPIVFEVFGH
-> ADSDGGDDSDKRSGESWKLITSLERKLPPSKLOTIVK
KGGLPSGKKREPIKMYQIPQRRRLSKDSKWVTISDLKIQA
VKEICYEVALNDFRHSRQEIEALAIVKMKELCAMTGKKDPN
ERDSWRAVARDVWDTYGVGDEKIEDMAYTGKGGTDVDLKV
HIDKLEDILQEVKKONNMKDEEIKVLRNKMLKMEKVLPLIG
SQEOKSQGSHKTKEPLVAGANSYSDNGVSKGESGELGKEER
VSQLMNGDDAFRRGKLEMMRODEJIFFKNLOQOEITKQLRRQ
NVPHREIPPENRKPRFPFKSNPKHRNSWSPGTHIITEDEV
IELAIPKDEGGRENKFRESQEKYGRAASEDVGSAMGTRSQD
HIOYSKGHLSNQPPPOLRWRSNSLNNGQPKTTRCQATASS
ESLNSHSGHPTADLQTFQAKRHIHQHRCPYCNYNTGGQVEG
STASCCQKGTDKPSHCNOFYTPPRMRRCFSAPNLKAGRETT
V (IN ISOFORM 3)
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MISSING (IN ISOFORM 3).

G -> V (IN REF. 1 AND 2
GGTL -> RGDI (IN REF. 4).

P -> S (IN REF. 4).

KL -> TW (IN REF. 3).

I -> V (IN REF. 3).

D -> G (IN REF. 4).

MW; E316EC295138E5DE CF
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Pred. No. 7.6e-81;
7; Mismatches 170;
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7 (IN ISOFORM 2 AND ISOFORM 3).
YESKLØALQRQVETRSLASETTEEEEEEEVEWTQHEFELA
QWAFRKWKSHQFTSLRDLLWGNAVYLKEANAISVELKKKVQ
FQFVLLTDTLYSPYEDLFDSEMEKTHEDRPFRTVYAVEV
QDLKNGATHYWSLDKLKGRLDLWGWLYDRAGEVASSAQDE
ETTMTGSDPFYDRFHWFKLVGSSPIFHGCVNERLADRTPSP
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SING (IN ISOFORM
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V (IN REF. 1 AND 2).
-> RGDI (IN REF. 1).
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Qy Db Qy	05 47 65
Qу	ISHLTDDELDALFDDVQKARAVRRGL :
Qy	02 NEDSDSQSSFP 712
Db .	: : :   28 TEEEEEEEEVP 73
11 50	LUT 5  LHUMAN KFIB.HUMAN STANDARD; PRT; 1816 AA. 060333; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last anontation update) Kinesin-like protein KIFIB (Klp).
	KIFIB OR KIANOS91. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;
	SEQUENCE FROM N.A. (ISOFORM 1). Bougueleret L., Dufaure-Gare I., Grel P.; "DNA encoding a kinesin-like protein (hklp) comprising bial
	53375, 26-0
	FROM N.A. (ISOFORM 2). , Takita J., Chen Y.Z., Soeda E., Piao H.Y., Has
R R R R R	"Cloning of human kiflb gene that maps at 1p36, which is homozygous deleted in neuroblastoma cell line NB1 and mutated in some other neuroblastoma cell lines."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
	RM 3). , Moon E., Chol W., Kim W.; man ortholog of mouse KiflB, a
	rication of the numan ortholog of mouse Killb, a kimily motor protein."; ed (JUL-2001) to the EMBL/GenBank/DDBJ databases.
	OF 479-1816 FROM N.A.
	781r
	<pre>ra N., Ohara O.; ilction of the coding sequences of unidentified humar</pre>
RT	<pre>lete sequences of 100 new cDNA clones from b large proteins in vitro.";</pre>
	Per 5-31-39/1998)

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RX KEDLINE-2128526; PubMed=11389829;
RA Zhao C., Takita J., Tanaka Y., Setou M., Nakagawa T., Takeda S.,
RA Zhao C., Takita J., Tanaka Y., Setou M., Nakagawa T., Takeda S.,
RA Zhao C., Takita J., Tanaka Y., Setou M., Nakagawa T., Takeda S.,
RA Yang H.W., Terada S., Nakata T., Takei Y., Saito M., Tsuji S.,
RA Hayashi Y., Hirokawa N.;
RT microtubule motor KIFHB-beta.";
RT microtubule motor KIFHB-beta.";
RT microtubule motor KIFHB-beta.";
RT Cell 105:587-597(2001).
CC -1- FUNCTION: MOTOR FOR ANTEROGRADE TRANSPORT OF MITOCHONDRIA. HAS A
CC MICROTUBULE PLUS END-DIRECTED MOTILITY.
CC -1- FUNCTION: MOTOR FOR ANTEROGRADE TRANSPORT OF MITOCHONDRIA. HAS A
CC MICROTUBULE PLUS END-DIRECTED MOTILITY.
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY FOUND ON THE VESICLE- AND
CC -1- SUBCLELLULAR LOCATION: PREDOMINANTLY FOUND ON THE VESICLE- AND
CC -1- SUBCLELLULAR ENTROCTURES WITHIN THE CYTOPLASM (BY SIMILARITY).
CC -1- SUBCLELLULAR ENTROCTURES WITHIN THE CYTOPLASM (BY SIMILARITY).
CC -1- DISEASE: Defects in KIF1B are a cause of Charcot-Marie-Tooth
CC Characterized by normal or slightly reduced nerve conduction
CC characterized by normal or slightly reduced nerve conduction
CC velocity and axonal loss with little evidence of demyelination or
CC hypertrophic changes in nerve biopstes.
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-104
                                                                                                                                                                                                                                                                    InterPro; IPR000253; FHA_domain
InterPro; IPR001849; PH.
InterPro; IPR001752; kinesin.
Pfam; PF00498; FHA; 1.
Pfam; PF00225; kinesin; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00233; PH; 1.
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SEQUENCE OF 1449-1816 FROM N.A.
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AX039604; CAC16629.1; -. EMBL; AF257176; AAK49332.1; -. EMBL; AY043362; AAK85155.1; -. EMBL; AB011163; BAA25517.1; -. EMBL; AK022977; BAB14341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         PROSITE; PS50003; PH_DOMAIN; Motor protein; Microtubules;
                                                                                                                                                         Alternative
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SIMILARITY: CONTAINS 1 FHA DOMAIN.
SIMILARITY: CONTAINS 1 PH DOMAIN.
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                                                                                              EDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ
                                                                                                                                                                                                                                                        FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG------GGAG----
                                               CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR
                                                                                                                                                                                                                                                                                           GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
                                                             SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS
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OWAFRKWKSHOFTSLROLLWGNAVY LKEANAISYELKKVO
FOFVLLTDILYSPLPPELLPTEMEKTHEDEPPRTVYAVEV
ODLKNGATHYWSLEKLKORLDLMREMYDRAGEMASSAQDES
ETTVTGSDPFYORFHWFKLVGSSPIFHGCVNERLADRYPSP
TFSTADSDITELADEQDEMEDFEDDEAFVDDAGSDAGTEEG
SDLESDGHDPFYDRSPWFILVGRAFYYLSNLLYFVPLIHRY
AIVSEKGEVRGFLRVAVØAIAADEEADDYGSGIROSGTAKI
SFDNEYKOSDFSVAMTRSGLSLEELRIVEGGGGSSEVIT
PPEEISRINDLDLKSSTLLDGKWYMEGFSEEIGHHLKLGSA
FTFRYTVLQASGILPEXADIFQGFHHRHDBAFSTEPLKN
NETTERSTUNYLEREFEL
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-> ANSDSGDDSDKRSCEESWKLITSLREKLPPSKLOTIVK
KCGLPSGKKREPIKMYQIPQRRKLSKDSKWYISDLKIQA
VKEICYEVALMDFRHSRQEIEALAIVKMKELCAMYGKKDPN
ERDSWRAVARDVWDTVGVGDEKIEDVMATGKGSTDVDDLKV
HIDKLEDILQFVKKQNNMKDEEIKVLRNKMLKMEKVLPLIG
SQEQKSFGSHKAKEPVGAGVSSTSENNVSKGDNGELAKJERR
VSQLMNGDPAFERGRLEWMRQEGIRFKNLQQGEITKQLERQ
NVPHRFIPPENRKPRFFFKSNPKHRNSWSPCTHIIITEDEV
                                                                                                                                                                                                                                                                                                                                        score 1623.5; Pred. No. 7.1e 127; Mismatches
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/TMH -> KIN (IN REF. 1).

D -> E (IN REF. 1).

R -> L (IN REF. 1).

VVY -> AVF (IN REF. 1).

ILATV -> NLSTE (IN REF. 1).

T -> I (IN REF. 1).

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SQDHIQVSKOHINNQQQPPQLRWRSNSLNNGQPKSTRCQAS
ASAESLNSHSGHPTADVQTFQAKRHIHQHRQSYCNYNTGGQ
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IDPLIDDYSGSGSKYLKDFQNNKHRYLLASENQRPGHFSTA
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/AR_011515.
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7.1e-79;
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; FALSE_NEG
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                      ROGERS K.R., Griffin M., Brophy P.J.;
"The secretory epithelial cells of the choroid
kinesin-related protein.";
Sumitted (AUG-1997) to the EMBL/GenBank/DDBJ-
--- SIMILARITY: CONTAINS 1 FHA DOMAIN.
--- SIMILARITY: BELONGS TO THE KINESIN-LIKE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFID_RAT STANDARD; PRT; 1097 AA 035787; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation updat
                                                                    InterPro; IPR000253; FHA_domain.
InterPro; IPR001752; kinesin.
Pfam; PF00498; FHA; 1.
Pfam; PF00225; kinesin; 1.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                        EMBL; AJ000696; CAA04248.1; -. HSSP; P17119; 3KAR.
                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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COILED COIL (POTENTIAL)
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InterPro; IPRO01752; kinesin
Pfam; PF00225; kinesin; 1.
Pfam; PF00169; PH; 1.
PFAM; PF00169; PH; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; KISC; 1.
SMART; SM00233; PH; 1.
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Neuron 6:113-122(1991) IN MICROTUBULE-ASSOCIATED TRANSPORT.
-!- FUNCTION: INVOLVED IN MICROTUBULE-ASSOCIATED TRANSPORT.
                                                                                                                                                                                                                                                                        DOMAIN
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; PROSITE; PS50003; PH_DOMAIN; 1. Motor protein; Cell division; Microtubulo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otsuka A.J., Jeyaprakash A.,
Hartshorne T., Franco R., Boj
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HSYWSFARNDPHFITQKQVYEELGVEMLEHAFEGYNVCIFAYGQTGSGKSYTMMGKANDP
                                     RSYMSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGK-- 123
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Faire K., Gruber D., Bulinski J.C.;
"Identification of kinesin-like molecules in myogenic cells.";
Eur. J. Cell Biol. 77:27-34 (1998).
-i- FUNCTION: MOTOR FOR ANTEROGRADE TRANSPORT OF MITOCHONDRIA. HAS
MICROTUBULE PLUS END-DIRECTED MOTILITY (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: PREDOMINANTLY FOUND ON THE VESICLE- AND
TUBULE-LIKE STRUCTURES WITHIN THE CYTOPLASM (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-10
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE~99023472; PubMed=9808286;
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PROSITE; PS0041; KINESIN_MOTOR_DOMAIN1; FALSE_NEG.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE; PS50006; FHA_DOMAIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DOMAIN
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nes 335; Conser
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SIMILARITY: CONTAINS 1 FHA DOMAIN.
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                                                                                                                                                                                                                                                                                                                  DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS
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ABLNETWEEKLRKTEAIRMEREALLAEMGVAIREDGGTLGVESPKKTPQVVNLNEDPLMS
                                                                                                                                                                                                                      -KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTSTLRYADRAKQ
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                                      RDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLA
                                                                      PGNFSTASMGSLTSS-PSSCSLNSQAGLTSVTSIQ--ERIMSTPGGEEAIERLKESEKII
                                                                                                         -GGGAGGSGGPVEESYPPDTPLEKQ-----IVSIQQPDATVKKMSKAEIVEQLNQSEKLY
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1 272 KINESIN-MOTOR.

360 381 COILED COIL (POTENTIAL).

451 483 COILED COIL (POTENTIAL).

538 618 FHA.

651 688 COILED COIL (POTENTIAL).

659 689 689 689 689 689 689; F64818C12FE69319 CRC64;
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Query Match
Best Local S
Matches 205
                                                           Motor protein;
DOMAIN 341
DOMAIN 620
NP_BIND 97
SEQUENCE 699
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01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Kinesin-II 85 kDa subunit (KRP-85/95 85 kDa
                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus (Purple sea urchin) Eukaryota; Metazoa; Echinodermata; Eleutherozoa; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P46872;
                                                                                                                                                                                   InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                            EMBL; L16993;
HSSP; P17119;
                                                                                                                                                                                                                                                                                                                           This
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                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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Nature 366:268-270(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cole D.G., Chinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
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                                                                                                                                                                                                                                                                                                                                                    II SUBFAMILY.
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 1 Similarity
205; Conser
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                                                                                PS0041; KINESIN_MOTOR_DOMAIN1; 1.
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Octell; Microtubules; AFP-binding; Coiled coil.
Octell; Microtubules; AIP-BINDING; Coiled coil.
1 340 KINESIN-MOTOR (BY SIMILARITY).
341 619 COILED COIL (BY SIMILARITY).
620 699 GLOBULAR (BY SIMILARITY).
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THE KINESIN-LIKE
Score 860; DB
Pred. No. 9e-39
88; Mismatches
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KF3B_HUMAN
    Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Bnuck D., Burrill W., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M. Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson
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15-DEC-1998 (
01-MAR-2002 (
Kinesin-like
                                                                                                                                                                                                                                                                                                                                        MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which cae code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015066;
                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                               FROM
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Metazoa; Primates; C
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
e protein KIF3B (Microtubule plus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GKSTHIPYRNSKLTRLLQDSLGGNAKTVMCANIGPAEYNYDETISTLRYAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Phillimore B.J.C.T., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plaub R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whittaker P., Willey D.L., Williams L., Williams M., Walms L., Williams M., Walms L., Whittaker P., Willey D.L., Williams L., Walliams M., Bentley D.R., Bec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB002357; BAA20815.1; -. EMBL; AL121897; CAC16425.1; -. HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence and comparative analysis of human chromosome Nature 414:865-871(2001).
-1-FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 603754;
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                                167
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                                                                                                                                                                                                                                                                                                    Match
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                                                                                                                                                                                                                                       6 NIKVVVRVRPFNAREIDRGAKCIVRME---GNQTILTPPPGAEEKARKSGKTIMDGPKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MICRÒTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR
MEMBRANOUS ORGANIELLES. PLUS END-DIRECTED MICROTUBULE SLI
ACTIVITY IN VITRO (BY SIMILARITY).
SUBUNIT: HETERODIMER OF KIF3A AND KIF3B (BY SIMILARITY).
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                    AFDRSY-WSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
WHDEETKMDTE----KVAKISLYDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAAL
                            REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK
                                                                                                                                                 TFDAVYDWN-----AKQFELYDETFRPLVDSVLQGFNGTIFAYGQTGTGKTYTMEGI 109
                                                                                                                                                                                                             SYRVYYRCRPMNGKEKAASYDKYYDYDYKLGQYSYKNPKGTAHEM------
                                                                                                                                                                                                                                                                          253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY
                                                                                                        -GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001752;
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85125
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POLY-GLY.
POLY-GLU.
POLY-SER.
POLY-SER.
W; 97FA4573AFA87023 (
                                                                                                                                                                                                                                                                                     Score 848.5; DB Pred. No. 4e-38;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                         -VRASYLETYQEETRDLLSKDQTKRLEL
                                                                                                                                                                                                                                                                       259;
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                                                                                                                                                                                                                                                                                                                                                  CRC64
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Lovell J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurone
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SLIDING
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Beck
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RESULT 11

KF3B_MOUSE

ID KF3B_M

AC Q61771

D7 15-JUL

D8 Mus mu

OC Eukary

OC Eukary

OC Eukary

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RA Yamaza

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15-JUL-1998 (1
15-JUL-1998 (1
Kinesin-like |
MOLOG 3B)
                                                                                                                                                                                                                                                                                                                                           Transport.";

J. Cell Biol. 130:1387-1399(1995).

-I- FUNCTION: MICROTUBULE-BASED ANTEROGRADE T
        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM TISSUE-Brain;
STRAIN-ICR; TISSUE-Brain;
MEDLINE-96032268; PubMed-7559760;
Yamazaki H., Nakata T., Okada Y., Hirokawa N.;
*KIF3A/B: a heterodimeric kinesin superfamily protein that
*KIF3A/B: a heterodimeric dinected motor for membrane organelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaria; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KF3B_MOUSE
Q61771;
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    657
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                                                                                                                                                                                                                                                                     ACTIVITY IN VITRO.
SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQS-----LLRHSYTNSQLGSPAPGRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAKTEEIHKEREAALEELGISIE----KGFVGPY----HSKEMPHLVNLSDDPLLAECLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKIMNRAFFDEEEDHWKLHPITRLENQQMMKRPVSAVGYKRPLSQHARMSMMIRPEARYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KRRETQQ--QMESRDEETLELKE--TYSSLQQEVDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKKMEDLRREKDAA-EMLGAKIKAMESKLLVGGKNIVDHTNEQQKILEQKRQEIAEQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EESYPPOTPLEKQIVSIQQPDATVKKMSKAEIVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VD-----GKSTHIPYRDSKLTRLLQDSLGGNAKTVMVANVGPASYNVEETLTTLRYANR
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                                                                                                                                                                                                                                                         SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
protein KIF3B (Microtubule plus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                               It is produced through a collaboration
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SLIDING
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Best Local
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SMART; SMOOL29; KISC; 1.

PROSITE; PSOO41; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

MOTOR_DOMAIN2; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

MOTOR_DOMAIN3; 1.

FOR SIMILARITY).

DOMAIN 346 579 COLLED COIL (BY SIMILARITY).

DOMAIN 346 579 GLOBULAR.

GLOBULAR.

GLOBULAR.

CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Motor protein; I
DOMAIN 346
DOMAIN 580
DOMAIN 580
NP_BIND 96
DOMAIN 394
DOMAIN 394
DOMAIN 723
SEQUENCE 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:107688; Kif3b.
InterPro; IPR001752; ki
Pfam; PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D26077;
HSSP; P17119;
                                                                                                                                                 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAFDRSY-WSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIKVVVRVRPFNARE----IDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKA
                                                                                                                                                                                                                                                                                                                                                                                               LADMSSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKERPDTGVYVKDLSSFVTKSVKEIEHVMNVGNQNRSVGATNMNEHSSRSHAIFVITI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRGDPEKRGVIPNSFDHIFTHISRSQNQQYL---VRASYLEIYQEEIRDLLSKDQTKRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVRVVVRCRPMNGKEKAASYDKVVDVDVKL--GQVSVKNPKG------
                                                                                                                                                                 NIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDK 571
                                                                                                                                                                                                                                                                                                                                                                                LVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VREHPSTGPYVEDLAKLYVRSFQEIENLMDEGNKARTVAATNWNETSSRSHAVFTLTLTQ
   DWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSF
                            NRSFFDDEEDHWKLHPITRLENQQMMKRPVSAVGYKRPLSQHARMSMMIRPEPRYRAEN-
                                                                                      LKKLFSKLQAVKAEIHDLQEEHIKERQELEQTQNELTRELKLKHLIIENFIPLEEKNKIM
                                                                                                                                                                                                       KKMEDLRREKDAA-EMLGAKIKAMESKLLVGGKNIVDHTNEQQKILEQKRQEIAEQ----
                                                                                                                                                                                                                                 AKTEEIHKEREAALEELGISIE----KGFVGPY----HSKEMPHLVNLSDDPLLAECLVY
                                                                                                                                                                                                                                                             EEEEGEEGEEDGDDKDDYWREQQEKLEIEKRA---IVEDHSLVAEEKM-----RLLKEKE
                                                                                                                                                                                                                                                                                               VE---
                                                                                                                                                                                                                                                                                                                        RAKNIKNKPRVNEDPKDALLREFQEEIARLKAQLEKRSIGRRKRREKRREGGGSGGGGEE
                                                                                                                                                                                                                                                                                                                                                   SAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGG------GGGAGGSGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWHDEETKMDTE---KVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTFDAVYDWN-----
                                                                                                                 PTRLRSGYRIILGDFHIFRFNHPEEARAERQEQS------LLRHSVTNSQLG------
                                                                                                                                               ----KRRETEIQQ--QMESRDEETLELKE--TYTSLQQEVDI------KTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                       ESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVE--QLNQSEKLYRDLNQTWEEKL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.0%;
nilarity 32.9%;
Conservative 11
                                                                                                                                                                                                                                                                                                                                                                               -GKSTHIPYRDSKLTRLLQDSLGGNAKTVMVANVGPASYNVEETLTTLRYAN
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                                                         SPAPGRHDRTLSKAGSDADGDSRSDS - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AKQFELYDETFRPLVDSVLQGFNGTIFAYGQTGTGKTYTMEG
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Pred. No. 6.6e-38;
6; Mismatches 25;
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FA369A4190EC8B47
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                          PLPHFRGKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TSHEMPKT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153;
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RESULT 12
KI21_STRPU
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Best Local Similarity
Matches 250; Conserv
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P46871;
01-NOV-1995
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                  NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urchin eggs.";
Nature 366:268-270(1993).
-!- SUBUNIT: TRIMER OF A 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                    PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

Motor protein; Microtubules; ATP-binding; Coiled coil.

Motor protein; Microtubules; ATP-binding; Coiled coil.

MOTOR_DOMAIN 1 337

KINESIN-MOTOR (BY SIMILARITY).

DOMAIN 338 613

COILED COIL (BY SIMILARITY).

DOMAIN 614 742

GLOBULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
Kinesin-II 95 kDa subunit (KRP-85/95 95 kDa s
                                                                                                                                                                                                                                                                                     PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                EMBL; U00996; AAA87393.1; -. HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus. NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scholey J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94050179; PubMed=8232586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                     InterPro; IPR001752; kinesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel heterotrimeric
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            111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     II SUBFAMILY
                                                                                                             | IKVVVRVRPFNAREIDRGAKCIVRMEGNQTI--LTPPPGAEEKARKSGKTIMDGPKAFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TMLLELDMPSRTTRDYEGPAISPKVQ--AALDAALQDEDEIQVDASSF 705
            NPELRGVIPNSFEHIFTHIARTQNQQFL----VRASYLEIYQEEIRDLLAKDQKKRLDLKE
                                E---HGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                        DTVYDWN---
                                                                   DRSY-WSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGK 12:
                                                                                                 VKVVVRCRPMNSKEISQGHKRIVEMDNKRGLVEVTNPKGPPGEPNKS------
                                                                                                                                                                                                                                                                                                           PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 AND 85 kDa
                                                                                                                                                                                                338
614
95
742
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                                                                                                                                            Conservative 122;
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BELONGS TO
                                                                                                                                                                                                  102
84202
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                                                                                                                                                      20.5%;
                                                     SKQIDLYDETFRSLVESVLQGFNGTIFAYGQTGTGKTFTMEGVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinesin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wedaman K.P., Hall K.,
                                                                                                                                                                                                   WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOCKED.
THE KINESIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kDa
                                                                                                                                                      Score 827.5; DB 1; Pred. No. 5.2e-37;
                                                                                                                                                                                                            ATP
                                                                                                                                                                                                  IP (POTENTIAL).
47C40A367BAA77B5 CRC64;
                                                                                                                                            Mismatches
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-I- FUNCTION: PROBABLY INVOLVED IN FLAGELLAR MAY PLAY A ROLE IN FLAGELLAR SYNTHESIS.
-I- TISSUE SPECIFICITY: FLAGELLAR AXONEME.
-I- SIMILARITY: BELONGS TO THE KINESIN-LIKE FIT SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                               MEDLINE=94299638; PubMed=8027176; Walther Z., Vashishtha M., Hall J.L.; "The Chlamydomonas FLA10 gene encodes
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67; KINESIN_MOTOR_DOMAIN2; 1.

MICTOTUBULES, ATP-binding; Coiled coil.

MICTOTUBULES KINESIN-MOTOR (BY SIMILARITY).

687 COILED COIL (POTENTIAL).

7 687 GLOBULAR (POTENTIAL).

8 786 GLOBULAR (POTENTIAL).

104 ATP (POTENTIAL).

8 391 POLY-GLY.

5 714 POLY-GLY.

5 714 POLY-ASP.
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Pred. No. 7.2e
30; Mismatches
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Best Local Similarity
Matches 253; Conser
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SEQUENCE
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Motor protein;
DOMAIN 1
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in Africa American visceral leishmaniasis." proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
-i- DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
-i- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-WHOM/BR/82 / ISOLATE BA-2;
MEDLINE-93133867; PubMed-8421715;
Burns J.M. Jr., Shreffler W.G., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00225; kinesin; SMART; SM00129; KISc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L07879;
HSSP; P17119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed S.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
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Eukaryota; Euglenoz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE;
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                      ----FQFDHVFWSVETPDACGATPATQADVFRTIGYPLVQHAFDGFNSCLFAYGQTGSGK
                                                                                                                                                                                                                             IKVVVRVRPFNARE--IDRGAKCIVRMEGNQTILTPP-----PGAEEKARKSGKTIMD
              NETSSRSHAVETLTL----TQKWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLK
                                                                                                                   NDRSSRSHAIIMLLLREERTMTTKSGETIRTAGKSSRMNLVDLAGSERVAQSQVEGQQFK
                                                  GKRKKGVKGGGEEVYVDVREHPSRGVFLEGQRLVEVGSLDDVVRLIEIGNGVRHTASTKM
                                                                             NPSTKG
                                                                                                     TYTMMGADVSALSGEGNGVTPRICLEIFARKASVEAQGHSRWIVELGYVEVYNERVSDLL
                                                                                                                                                                               GPKAFAFDRSYWSF---DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGK 114
                                                                                                                                                                                                         VKVSVRVRPLNERENNAPEGTKVTVAAKQAAAVVTVKVLGGSNNSGAAESMGTARRVAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS0041; KINESIN_MOTOR_DOMAIN1; 1.
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Octein; Microtubules; ATP-binding; Coiled coil; Repeat.
1 399 KINESIN-MOTOR (BY SIMILARITY).
426 >955 COILED COIL (POTENTIAL).
122 129 ATP (POTENTIAL).
704 >955 7 X 39 AA APPROXIMATE TANDEM REPEATS.
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28.1%;
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Pred. No. 3.9e
25; Mismatches
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No. 3.
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RESULT 15

KF3A_MOUSE
ID KF3A_M
AC P28741
DT 01-DEC
DT 01-DEC
DT 01-DEC
DT 15-JUL
DE Kinesi
DE Motor
GN KIF3A
OS MUS MUU
OC EUKARY
OC MAMMAI
ON NCBLIN
RR FEQUEN
RR ALZAWA
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RR ALZAWA
RR JISUE
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RC 1-- FU
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A Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hir A Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hir R., Kinesin family in murine central nervous system.";
L J. Cell Biol. 119:1287-1296(1992).
C -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR CONTROL OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           motor 3A).

KIF3A OR KIF3.

Mus musculus (Mouse).

Eukaryota; Metazoa; Ch

Mammalla; Eutheria; Ro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE-Brain;
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                                                                          SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASQLEATAAA------KMSAEQDRENTRATLEQQLRDSEERAAELASQLESTTAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTAAERDQLLQQ--LTELQSERTQLSQVVTDRERLTR-DLQRIQYEYGETELARDVALCA
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Rodentia;
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                                                                  TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ARESACERLTSLE
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; Murinae; Mus
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564	527 TQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMV	Qy
568	524 EQERLDIEEKYTSLQEEAQGKTKKLKKVWTMLMAAKSEMADLQQE	Db
526	ELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGC	Qy
523	464 QQEHQSLLEKLSALEKKVIVGGVDLLAKAEEQEKLLEESNMELEERRRRAEQLRKELEEK	Дb
472	RDLNQTWEEKLAKTEEIH	Qy
463	: : : : : : : : : : : : : : : : : : :	Db
421	408SYPPDTPLEKQIVS	Qy
403	344 NIKNKARINEDPKDALLRQPQKEIEELKKKLEEGEEVSGSDISGSEEDDEEGELGEDGEK	Db
407	358 RIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGG-GGGGAGGSGGPVEE	QΥ
357 343	296 MSSGKOKKNOLVPYRDSVLTWLLKOSLGGNSMTAMLAALISPADINPEETLSTLRYADSAK  GKSTHVPYRNSKLTRLLQDSLGGNSKTMMCANIGPADYNYDETISTLRYANRAK 290GKSTHVPYRNSKLTRLLQDSLGGNSKTMMCANIGPADYNYDETISTLRYANRAK	Db Qg
289	33 KG	Db
297	238 KWHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALAD	Qy
232	173 ERPDVGVYIKDLSAYVVNNADDMDRIMTLGHKNRSVGATNMNEHSSRSHAIFTITIECSE	Db
237	T	Qy
-		Ъ
179	123 KEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVR	QУ
114	62 TEDTVFGPE-SKQLDVYNLTARPIIDSVLEGYNGTIFAYGQTGTGKTFTMEGVR	ДЪ
122	63 AFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG	Qy
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63	GAKCIVRMEGNOTTI.TPPPGAEEKARKSGKTINDG	QΨ
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	442 445 POLY-GLU. 509 512 POLY-ARG.	FT
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	351 586 COILED COIL (BY SI	7 F
	Microtubules; ATP-binding; Coiled coil; Ne 350 KINESIN-MOTOR /BY STMTLARTTY	T X
	TE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.	DR.
	HEAVI.	
	Pfam; PF00225; kinesin; 1.	
	MGD; MGT:107689; Kif3a. InterPro; IPR001752; kinesin.	
	HSSP; P17119; 3KAR.	
	MBL; D	
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Maximum Match 100%
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1: sp_barchea:*

2: sp_bungd:*

4: sp_human:*

5: sp_human:*

5: sp_mammal:*

7: sp_mhc:*

8: sp_organel1.

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:

12: sp_vtrus:*

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17: sp_archeap
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sp_bacteria:*
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sp_virus:*
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O9v7t6 drosophila
O9nbl1 drosophila
O18778 caenorhabdi
O9ng92 dictyosteli
O9ng92 dictyosteli
O9eqw7 mus musculu
O9h193 homo sapien
O9h194 homo sapien
O9h1h8 homo sapien
O9h1h9 homo sapien
O9ng18 homo sapien
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O9v7c9 drosophila
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O9v888 caenorhabdi
O15058 homo sapien
O09997 caenorhabdi
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17.9	18.1	18.3	18.3				18.6				19.0	19.1	19.2	19.3	19.4	19.4	19.8	19.8	20.0	21.0	24.3	24.9	25.3	25.7	25.7	25.7	25.7	26.7
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	Q9lut5 arabidopsis	Q9u179 leishmania	_	Q9u921 tetrahymena	Ξ	-	Ç,	Q965t6 caenorhabdi	_	Q9u142 leishmania			5 arabido		drosoph11		_		8 mus	homo	homo				016866 drosophila		irosophil	Q9dda6 xenopus lae

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## ALIGNMENTS

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KA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., McDarry C., McTeod M.P., McShrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.K., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Reinert K., Remington K.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Turner R., Venter E., Wang X.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RMBL, AE003805; AAF57957.1; -.
PR HSSP; P17119; 3KAR.
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Matches 367; Conservative
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 1773 AA; 200755 MW; 335BE9CD5E4DB681 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00498; FHA; 1.
Pfam; PF00225; kinesin; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
SMART; SM00233; PH; 1.
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InterPro; IPR001752; kine
InterPro; IPR001849; PH.
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                                                                                                                 NIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFD 65
                                                                                                                                                                                                                                                         TGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEE
                                                                                                                                                                                                                                                                                                                                                                            RSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKE- 124
                                                                                                                                                                                                                                                                                                                                                                                                                        SYKVAVRVRPFNSREIARESKCIIEWAGATTAITNP-----KVPPNTSDSVKRFNFD 83
 CEKRDANKDELTKSTVIKSPTKSRNRNGSTTEMAVDQLQASEKLIAELNETWEEKLKRTE
                                                                                                                                                                                                                                         LGPYVEDLSKLAVTDYQDIHDLIDEGNKARTVAATNMNETSSRSHAVFTIFFTQRRHDLM 262
                                                                                                                                                                                                                                                                                                                                                             YSYWSHDHHDADFSTQSMVYKDIGEEMLQHSFDGYNVCIFAYGQTGAGKSYTMMGRQEEQ
                                                         KAVVNEDANAKLIRELKEEIQKLRDLLKAEG
                                                                         HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGGFVEESTPPDTPLEKQIVS
                            IQQPDATVKKMSKAEI----
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Pred. No. 3
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                             -----VEQLNQSEKLYRDLNQTWEEKLAKTE
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3.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193;
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                                                            IEVQEGPDGK----VV
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Qy
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Best Local Similarity
Matches 364; Conser
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Eukaryota; Metazc
Pterygota; Neopte
Ephydroidea; Dros
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                Grossberger R., Saxton W.M., Dickson B.J.;
"Characterization of the Drosophila Uncl04/KIF1A homolog,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF247761; AAF74192.1; -....
HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINESIN SUPERFAMILY MEMBER DUNC104. UNC-104 OR CG8566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09NBL1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
ATP-binding; Coiled coil; Microtubules; Motor SEQUENCE 1671 AA; 189430 MW; EAC3F1D30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9NBL1
                                                                                                                                                                                                                    PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISc; 1.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                        Pfam; PF00498; FHA; 1.
Pfam; PF00225; kinesin; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0034155; unc-104.
InterPro; IPR000253; FHA_domain.
InterPro; IPR001752; kinesin.
InterPro; IPR001849; PH.
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                                             NIKVVVRVRPFNAREIDRGAKCIVRMEGNOTILTPPPGABEKARKSGKTIMDGPKAFAFD
  RSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKE-
                              SVKVAVRVRPFNSREIARESKCI IEMAGATTAITNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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                                                                                Conservative
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                                                                                              40.5%;
                                                                                  141;
                                                                                Score 1630.5; DB
Pred. No. 6.2e-86;
1; Mismatches 188
                                                                                                                                                   EAC3F1D3022360AF CRC64;
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                                                                                  188;
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                                KVPPNTSDSVKRFNFD
                                                                                    Indels 129;
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                                                                                                          Length
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                                                                                                                Q18778 PRELIMINARY; PRT Q18778; O1-NOV-1996 (TrEMBLrel 01, Creat 01-DEC-2001 (TrEMBLrel 19, Last 01-DEC-2001 (TrEMBLRel 19, Last HYPOTHETICAL 179.4 KDA PROTEIN. C52E12.2
                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                              None;
*Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium. Science 282:2012-2018(1998).
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                                      PubMed-9851916;
                                                                                               Nematoda;
                                                                                     da; Chromadorea;
Caenorhabditis.
                                                                                                                                    Last
                                                                                                                                                     Created)
                                                                                                                                             Last
                                                                                                                                                                                                                       -KEANAISVELKKKVQFQ
                                                                                                                                  sequence update) annotation update)
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                                                                                             Rhabditida; Rhabditoidea;
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Best Local Sim
Matches 356;
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SEQUENCE FROM N
STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Direct Submission.";
Submitted (SEP-2001) to the
EMBL; U50135; AAA93453.2; -.
Hypothetical protein.
SEQUENCE 1581 AA; 179408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2; Waterston R.;
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                                                                                                                                                       WFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRR-----
                                                                                        GEAILELHCEFINEDGNVTLTMKPNASCYINGKQVTTPTVLHTGSRVILGEHHVFRYNDP
                                                                                                                              GSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHP
                                                                                                                                                                                                                                               HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGFVEESYPPDTPLEKQIVS
                                                                                                                                                                                                                                                                                    OKKNO-LVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN
                                                                                                                                                                                                                                                                                                                           ETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGK
                                                                                                                                                                                                                                                                                                                                                                STGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
SLLEFPEELKWTSDQ--KRVVLKAAIKWRYHQFTSVRDDLWGNAIFV----
                   SQSSFPVRDKYMSNGTIDNFSLDTAITMP----GTPRSDDDGDALFFGDKKSKQDASNVD
                                                                            QEARQSRHNLAAIAEQPIDWKYA-----QQELLDKQGIDLKADMEK----
                                                                                                                                                                                              VQETPGKHKKGPKLPAHVHEQLEKLQESEKLMAEIGKTWEQKLIHTEEIRKQREEELRDM
                                                                                                                                                                                                       QAVVNEDPNAKLIRELNEEVIKLRHILKDKG---------IDVTD
                                                                                                                                                                                                                                                                           KKSNKGVIPYRDSVLTWLLRENLGGNSKTAMLAALSPADINFDETLSTLRYADRAKQIVC
                                                                                                                                                                                                                                                                                                                                                       {\tt LLGPYVDDLTKMAVCSYHDICNLMDEGNKARTVAATNMNSTSSRSHAVFTIVLTQKRHCA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVKVAVRVRPFNQREISNTSKCVLQVNGNTTTI------
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(MAR-1996)
                                      RREKVE----LEQKMYHQT-REYESMIENLQKQVDLAQSYISGGGSIWEGERMLTS
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1581 AA; 179408 MW;
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EMBL/GenBank/DDBJ
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No. 1.26
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 -KEANAIS
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RESOLATION OF THE PROPERTY OF 
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Best Local Similarity
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Q9NGQ2;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
SMART; SM00129; KISC; 1.
SMART; SM000233; PH; 1
PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE: PS00067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE: PS500067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 2205 AA; 248002 MW; 02C5101E9D61C9ED CRC64;
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MEDLINE-20014990; PubMed-10545495;

MIDLINE-20014990; PubMed-10545495;

POLIOCK N., de Hostos E.L., Turck C.W., Vale R.D.;

PREconstitution of membrane transport powered by a novel dimeric kinesin motor of the Uncl04/KIF1A family purified from Dictyostelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001752; kinesin.
InterPro; IPR001849; PH.
Pfam; PF00225; kinesin; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pollock N., Vale R.D.;
Submitted (MAR-2000) to the
EMBL; AF245277; AAF63384.1;
HSSP; P17119; 3KAR.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                         KQKKNQLYPYRDSYLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN
                                                                                                                                    PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD
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                                                                                                  KTRGTAIDRVSKISLVDLAGSERANSTGATGVRLKEGANINKSLSTLGKVISALAENST-
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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45.1%;
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                          Pfam; PF00225; kinesin; 1.

PRINTS; PR00380; KINESINHEAVY.

SMART; SM00240; FHA; 1.

SMART; SM00129; KISC; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

ATP-binding; Colled coll; Microtubules; Motor SEQUENCE 1749 AA; 195812 MW; DAE9E026127DD
                                                                                                                                                                                                                                  Plasma Membrane through Direct Cell 103:569-581(2000). Cell EMBL, AB037923; BAB16346.1; -. HSSP; P33176; 1BG2.
                                                                                                                                                                                                                                                                                                                      STRAIN=ICR; TISSUE-BRAIN; MEDLINE-20560742; PubMed=11106728;
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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InterPro; IPR001752; kinesin.
                                                                                                                                                                                                                         MGD; MGI:1098264; Kifl3a.
                                                                                                                                                                                                                                                                        "A Novel Motor, KIF13A, Transports Mannose-6-Phosphate Receptor "A Novel Motor, KIF13A, Transports Mannose-6-Phosphate Receptor Plasma Membrane through Direct Interaction with AP-1 Complex.";
                                                                                                                                                                                                                                                                                                  Hirokawa N.;
                                                                                                                                                                                                                                                                                                            Nakagawa T., Setou M.,
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VKVAVRVRPMNRRELELNTKCVVEMEGNQTVLHPPPSNTKQGERK-----PPKVFAFDY
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                                                            Similarity
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Chordata; (
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Last sequence update)
Last annotation update)
                                                            Score 1468;
Pred. No. 1
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Q9H193;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
        TISSUE-FETAL BRAIN;
Jamain S., Quach H., Fellous M., Bourgeron T.;
Jamain S., Quach H., Fellous M., Bourgeron T.;
Identification of the human KINESIN-13A gene, homologous
Drosophila kinesin-73 and candidate for schizophrenia.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ291579; CAC20443.1; -.
HSSP; P33176; 1BG2.
                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
                                                                                                                                                     KINESIN-13A2
                                                                                    SEQUENCE
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IPR000253;
IPR001752;
                                                                                                            Chordata;
Primates;
FHA_domain kinesin.
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19,
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Last annotation updat
                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 343
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PRINTS; PR00380; KINESINHEAVY.

SMART; SM00240; FHA; 1.

SMART; SM00129; KISC; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

ATP-binding; Coiled coil; Microtubules; Motor protein.

ATP-binding; Coiled coil; Microtubules; Motor CRC64;

SEQUENCE 1749 AA; 196070 MW; F4C1C2E8435D578D CRC64;
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REQLVKA
                    EEALKTA
                                            RLAYSS
                                                                RDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEELRQQQAQM
                                                                                       MKTLNSNDPVQNVV-QVLEKQYLEEKRSALEEQRLMYERELEQLRQQLSPDRQPQSSGPD
                                                                                                     SAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNE----
                                                                                                                                      D----FEKETGPP---EHD-----LDAASEASSE-----PDYNYEFAQMEVI
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                                                                                                                                                                                  IDIASDGDVTLTPKENARSCVNGTLVCSTTQLWHGDRILWGNNHFFRINLPKRKRRDWLK
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No. 2
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.6e-76;
                                           -QQKVTQWAEERD-ELFRQSLAKL
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                                                                                                               -DSDSQSSFPV
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RESULT Q9H194 ID Q9

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InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
ATP-binding; Coiled coil; Microtubules; Motor protein.
ATP-binding; Coiled coil; Microtubules; Motor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jamain S., Quach H., Fellous M., Bourgeron T.;
"Identification of the human KINESIN-13A gene, homologourosophila kinesin-73 and candidate for schizophrenia.",
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AJ291578; CAC20442.1; -.
HSSP; P33176; 1BG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-MAR-2001
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IDIASDGDVTLTPKENARSCVNGTLVCSTTQLWHGDRILWGNNHFFRINLPKRKRRDWLK
                                                                                                         VNEDPNAKVIRELREEVEKLREQLSQA------
                                                                                                                                                                                                                                                                                                                                 GLIPRLCCALFKRIS-LEQNESQTFKVEVSYMEIYNEKVRDLLDPKGSRQSLKVREHKVL
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                                               -GIKVGDDKCYLVNLNADPALNELLVYYLK-DHTRVG--
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43.6%;
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Pred. No. 2.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                            -ADTSQDIQLFGIGIQPQHCE
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phrenia.";
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Q9H1H8;
Q9H1H8;
O1-MAR-2001 (TrEMBLrel. 16, C
O1-MAR-2001 (TrEMBLrel. 16, L
O1-DEC-2001 (TrEMBLrel. 19, L
KINESIN-LIKE PROTEIN RBKINZ.
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InterPro; IPRO00752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00129; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
ATP-binding; Coiled coil; Microtubules; Motor CRC64;
SEQUENCE 1770 AA; 198550 MW; D926CDD8ED8CB3IC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 6p containing a novel kinesin-like gene, F submitted (NOV-2000) to the EMBL/GenBank/DDBJ databas EMBL; AY014404; AAG38891.1; -
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P33176; 1BG2.
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TISSUE-RETINA;
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                     KMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSGKQK
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O1-MAR-2001 (TIEMBLIEL 16, C.
O1-MAR-2001 (TIEMBLIEL 16, L.
O1-DEC-2001 (TIEMBLIEL 19, L.
KIMESIN-LIKE PROTEIN RBKINI.
                                                                                                                                                                                                                                                                                                                                                 Chen D., Squire J.A., Gallie B.L.;
"Genomic amplification in retinoblastoma narrowed to 1.2 Mb chromosome 6p containing a novel kinesin-like gene, RBKIN.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY014403; AAG38890.1; -...
HSSP; P33176; 1BG2.
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Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'`rvota; Primates;
                                                                                                                                                PRINTS; PRO0380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00129; KIS; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
ATP-binding; Coiled coil; Microtubules; Motor CRC64;
SEQUENCE 1805 AA; 202258 MW; ABF249E859A04B7A CRC64;
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InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
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                                                                                                SEQUENCE FROM N.A.

MEDLINE-20435838; PubMed-10859302;

Hanada T., Lin L., Tibaldi E.V., Reinherz E.L., Chishti A.H.;

"GAKIN: a novel kinesin-like protein associates with the human momologue of the Drosophila discs large tumor suppressor in T
lymphocytes.";
J. Biol. Chem. 275:28774-28784(2000).
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Best Local S
Matches 318
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R InterPro; IPR000253; FHA_domain.

R InterPro; IPR000253; FHA_domain.

R InterPro; IPR00025; kinesin.

R Pfam; PP01025; cAP_GLY; 1.

R Pfam; PP00225; kinesin; 1.

R Pfam; PP00225; kinesin; 1.

R Pfam; PP00225; kinesin; 1.

R Pfam; SM00240; FHA; 1.

R PRINTS; PR00380; KINESINHEAVY.

R SMART; SM00129; KISC; 1.

R SMART; SM00129; KISC; 1.

R PROSITE; PS00845; CAP_GLY; 1.

R PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PS00411; KINESIN_MOTOR_DOMAIN2; 1.

R PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 001349
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les 318; Conserv
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                                                                           SDWFYARREAASAILGLDQKISHLTDDELDALFDDDVQKARAVRRGLYEDNE
                                                                                                                                                                  LKEHCTFE-NVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRENHP-EE
                                                        -NYEYAQMEVTMKALGSNDPMQSIL-NSLEQQHEEEKRSALERQRLMYEHE
                                                                                                        KKAEREDEDQDPSMKNENSSEQL
                                                                                                                                                    LPEHCIIDITSEGQVMLTPQKNTRTFVNGSSVSSPIQLHHGDRILWGNNHFFRLNLPKKK
                                                                                                                                                                                                   SLQSS--GIKYGDDKCFLVNLNADPALNELLVYYLKE-HTLIGSANSQ---DIQLCGMGI
                                                                                                                                                                                                                  SIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKI
                                                                                                                                                                                                                                                              IVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGI
                                                                                                                                                                                                                                                                                               LYDAKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINESLTTLGLVISALADQ
                                                                                                                                                                                                                                                                                                                                                                                                            GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                              REHSVLGPYVDGLSKLAATSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVLKITLTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK
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PRELIMINARY;
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                                                                                                                                                                                                                                                  ----EAMKSPELKDRLEESEKLIQEMTVTWEEKLRKTEEIAQERQKQLESLGI
                                                                                                                  LLRHSVINSQLGSPAPGRHDRTLSKAGSDADGDSRSD-SPLPHFRGKD::: :: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114;
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Pred. No. 3.3e-73;
L4; Mismatches 193;
PRT;
1921
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A Li H.P., Liu Z.M., Nitrenberg M.;

Trinsin-73 in the nervous system of Drosophila embryos."

Proc. Natl. Acad. Sci. U.S.A. 94:1086-1091(1997).

R EMBL; U81788; AAB50404.1; -.

R HSSP; P33176; 1B62.

R FlyBase; FBg00019968; Khc-73.

R Interpro; IPR000938; CAP-Gly.

R Interpro; IPR001253; FHA_domain.

R Interpro; IPR001253; Kinesin.

R Interpro; IPR001253; Kinesin.

R Interpro; IPR001253; Kinesin.

R Interpro; IPR00125; Kinesin.

R Interpro; IPR00125; Kinesin.

R Interpro; IPR00125; Kinesin.

R Interpro; IPR00125; Kinesin.

R Ffam; PF00130; CAP-GLY; 1.

R PFAMT; SM00240; FHA; 1.

R PRINTS; PR00380; KINESINLMOTOR_DOMAINI; 1.

R PROSITE; PS00411; KINESIN_MOTOR_DOMAINI; 1.

R PROSITE; PS00411; KINESIN_MOTOR_DOMAINI; 1.

R PROSITE; PS00411; KINESIN_MOTOR_DOMAINI; 1.

R PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.

R PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.

R PROSITE; PS0041A; 215047 MW; 4643F6F9783E99DO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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KHC-73 OR CO
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01-JUL-1997
01-JUL-1997
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Li H.P., Liu Z.M., Nirenberg M.;
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                                                IKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDR
                                                                                                                                                 PYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHDEETK
                                                                                                                                                                                                                                                                                                                SYMSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYGKEHG
                                                                                                                                                                                                 PYVDGLSQLAVTSYQDIDNLMTEGNKSRTVAATNMNAESSRSHAVFSVVLTQILTDQATG
                                                                                                                                                                                                                                                 IIPRLCDQLFSAIAN-KSTPELMYKVEVSYMEIYNEKVHDLLDPKPNKQSLKVREHNVMG
                                                                                                                                                                                                                                                                                                  CFYSLNPEDENFASQETVFDCVGRGILDNAFQGYNACIFAYGQTGSGKSYTMMGTQESKG
                                                                                                                                                                                                                                                                                                                                                  IKVAVRVRPFNRREIELDTKCIVEMEKQQTILQNPPPLEKIERKQ------PKTFAFDH
                                                                                                                                                                                                                                                                                                                                                                                                          305;
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-GDVQDKLAESENLMKQISQTWEEKLVKTERIQNERQQALEKMGISVQAS
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                      Score 1396.5;
Pred. No. 2.8e
98; Mismatches
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RA Addms D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Golzyne J.D.,
RA Adams D., Celniker S.E., Holt R.A., Ashlurner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Buttis M.F., Apbayani A., An H.-J., Andrews Ffannkoch C., Baldwin D.,
RA Bulliw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles M.D.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kandan T.J., Herrandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mensulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mang Z.-Y., Wassarman D.A., Weisnen D.R., Pacleb J.M.,
RA Rainert K., Remington K., Staunders R., D.C., Scheeler F., Shen H.,
RA Rainert K., Remington K., Staunders R., D.C., Scheeler F., Shen H.,
RA Rainer E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Harlsa R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Harlsa R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ra Rainer E., Lei S., Shan M., Zhang G., Zhao Q., Zheng L.,
Ra Rainer B. R., Royler G.M., Shan M., Zhang
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    Q9V7C9
Q9V7C9;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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KHC-73 OR CG8183.
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01-JUN-2001
                                    HSSP; P33176; 1BG2
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                                                        AE003810;
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                    FBgn0019968;
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Q20888 Q20888; 01-NOV-1996 ( 01-JUN-2001 ( 01-DEC-2001 ( HYPOTHETICAL

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(TrEMBLrel. 01, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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SMART; SM00240; FHA; 1.

SMART; SM00129; KISC; 1.

PROSITE: PS00845; CAP_GLY; 1.

PROSITE: PS00841; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE: PS0067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE: PS0067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE: PS0067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.

ATP-binding; Coiled coil; Microcubules; Motor protein.

ATP-binding; Coiled coil; Microcubules; Motor Protein.

SEQUENCE 1921 AA; 214997 MW; DEDCA75A63444C42 CRC64;
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InterPro; IPR001752; kinesin.
InterPro; IPR001220; Lectin_legB
Pfam; PF01302; CAP_GLY; 1.
Pfam; PF00225; kinesin; 1.
558
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SYWSFDKNAPNYARQEDLFQDLGVPLLDNAPKGYNNCIFAYGQTGSGKSYSMMGYGKEHG 126
EPQTPAQLIDYNFARDEIMQNELSN
                         -- EARAERQEQSLLRHSVTNSQLGS
                                                                                                                         VGPYHSKEMPHLVNLSDDPLLAECLYYNIKPGQTRVGNVNQDTQAEIRLNGSKILKEHCT
                                                                                                                                                                                PDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEKGF
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                                                     ITIEDSGLYMEPVQGARCFVNGSAAVEKTPLQNGDRILWGNHHFFRVNSPKSNNTSMCAS
                                                                             FENVDNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPE---
                                                                                                                                                                                                                                                                            NDKFVPYRDSVLTWLLKDNLGGNSRTVMVATISPSADNYEETLSTLRYADRAKRIVNHAV
                                                                                                        -GIKVEKNKYYLVNLNADPSLNELLVYYLKDRTLIGGRTISGQQPDIQLSGLGIQPEHCV
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Pred. No. 2.8
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171; Indels
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"The sequence of C. e submitted (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode investigating biology. The C. ele Science 282:2012-2018(1998).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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SMART; SM00129; KISC; 1.
PROSITE; BS50067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE; BS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO00253; FHA_domail
InterPro; IPRO01752; kinesin.
Pfam; PF00225; kinesin; 2.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U41536; AAK39239.1;
HSSP; P33176; 1BG2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2001) to
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                                                 MDTEKVAKISLVDLAGSERATSTGATGARLKEGAEIN-----
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                                                                                                                                              VYVFINQKLDFRSLTTLGMVISALAERNS---
                                                                                                                                                                                                                                                                                                                                 PMVDGLSILAVNSFEQISNLLEEGNKSRTVAATNNNAESSRSHAVESLIVTQTLHDLENG
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GGGGGGAGGSGGPVEESYPPDTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDL
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NCE 1595 AA; 179401 MW;
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kinesin.
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EMBL/GenBank/DDBJ
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Pred. No. 6.8e-66;
0; Mismatches 217;
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01-NOV-1996 (Tremi
01-DEC-2001 (Tremi
KIAA0042 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-96051398; PubMed-7584044;

MEDLINE-96051398; PubMed-7584044;

Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., S
Seki N., Kawarabayashi Y., Ishikawa K., Tabata S.;

**Prediction of the coding sequences of unidentified human
The coding sequences of 40 new genes (KIAA0041-KIAA0080) d
analysis of cDNA clones from human cell line KG-1.*;

DNA Res. 1:23-229(1994).
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Q15058
pfam; pf00498; FHA; 1.
pfam; pf0025; kinesin; 1.
prints; pr00380; kinesin; 1.
prints; sm00240; FHA; 1.
smart; sm00240; FHA; 1.
smart; sm00129; kisc; 1.
prosite; ps00411; kinesin_motor_domain1; 1.
prosite; ps00411; kinesin_motor_domain2; 1.
prosite; ps50067; kinesin_motor_domain2; 1.
prosite; ps50067; kinesin_motor_domain2; 1.
stplittled coil; microtubules; Motor protein.
stplittled coil; microtubules; Motor protein.
stplittled coil; microtubules; Motor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA0042
                                                                                                                                                                                                                                                 InterPro; IPR000253; FHA_domain.
InterPro; IPR001752; kinesin.
InterPro; IPR001854; Ribosomai_L29
                                                                                                                                                                                                                                                                                                                                    EMBL; D26361; BAA05392.1; HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTWEEKLAKTEETHKEREAALEELGISIEKGFVGPYHSKEMPHLVNLSDDPLLAECLVY
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Query Match Best Local S Matches 281

Similarity

29.1%; So 34.8%; Pi itive 152;

Score 1174.5; DB Pred. No. 1.7e-59; 52; Mismatches 239

239; 4;

Indels Length

135;

Gaps

17;

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281;

Conservative

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RESULT
ID 9997
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Q09997;
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Q1-NOV-1996
Q1-JUN-2001
PUTATIVE KINI
                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBI_TaxID=6239;
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STRAIN-BRISTOL N2:
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996 (TrEMBLrel. 01, Last sequence update)
001 (TrEMBLrel. 17, Last annotation update)
KINESIN-LIKE PROTEIN R144.1 IN CHROMOSOME
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Matches 281
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InterPro; IPR001753; klnesin.
Pfam; PF00225; klnesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Hypothetical protein;
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Submitted
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SEQUENCE 928 AA;
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Submitted (FEB-1999) to the
EMBL; U23515; AAK21452.1; -
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Ali M.Y., Khan S.T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFAFDRSYWSFD-----KNA------PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQ
 NHLYVENNPTKKG
                                                                  QAEIRLNGSKILKEHCTFEN-VDNVVTIVP-NEKAAVMVNGVRIDKPTRLRSGYRIILGD
                                                                                                                                                                                  SYPPOTPLEKQIVSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHK 467
                                                                                                                                                                                                                               STLRYADSAKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGFVEE
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                                                  GNF I QMSGLS I LPQHVT LKNDGNNQ I HLSPCSEDLD I FINGKPVHGETQLQQNDRVFFGG
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                         FHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSD---
                                                                                                       HASGASEKVEMEAKK-----KKMCHLWNLNEDPALTNVIVHFIPVGESVVGNKPTSS
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Similarity 38.8%;
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## ALIGNMENTS

JOURNAL MEDLINE REFERENCE REFERENCE AUTHORS TITLE DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1
HAAXTRSYV
LOCUS COMMENT AUTHORS TITLE JOURNAL Furlong, R.A.

Furlong, R.A.

Direct Submission

Submitted (16-AUG-1995) R.A. Furlong, University of Cambridge, Submitted (16-AUG-1995) R.A. Furlong, University of Cambridge, Of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK

Overlaps with M78444, M78705, T07754, T15633 and T77291. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6972)
Furlong,R.A., Zhou,C.Y., Ferguson-Smith,M.A. and Affara,N.A. Characterization of a kinesin-related gene ATSV, Within the tuberous sclerosis locus (TSC1) candidate region on chromosome 90: 96299637
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/dev_stage="foetal"
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    TGAGTGCCTGCTCTACTACATCAAGGATGGGATCACCAGAGTGGGCAGGGAGGATGGCGA
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Grossberger,R., Saxton,W.M. and Dickson,B.J.
Characterization of the Drosophila Uncl04/KIFIA homolog, DUncl04
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ELTKSTVIKSPWSKNIRKGSTYEMAVDOLQASEKLIRELNEWEEKIKRTEEIRVQRE
AVFÆRKOVAKEDGITYGVFSPKKTPHLVNLAEDDRISECLLYYIKGGITRIGTHEA
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VPQDIQLSGSHILKEHCTFENKNSTVTLLPHKDAIIYVNGRKLVEPEVLKTGSRVILG
KNHVFRTNPEQARELDRIETENAEREVEKTDQOVMNFRACELLEKGGIDLKAE
MKRKLDNLESDYKREKLQADQOFEORKTYEARIDALGKOVEEGSMTIMSMYSSYSPED
FHQEEDVYTNPMYESCWTAREAGLAMAFRKWRYHQFTSLRDDLWGNAIFLKEANAIS
YELKKKYQFQFTLLTDTLYSPLPPELASTVAFVHQEDEFGAPPSKTLVAVETDTKN
GATHHWSLEKLRQRLEILMREMYNHEAEMSPTSPDINVESTGDPFNGFWFRWYGR
SFIYLSNLLYPVPLVHKVAIVNERGDVBGYLRIAVQFVLDEESIDFNNGVKQSARLVF
NEDDAKFKYRALNEKDDVGKYLDNGGLDSKLEELEVVDSGRGLDSNASGEGENSEEE
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SDSVKRFNFDYSYWSHDHHDADFSTQSMVYKDIGEEMLQHSFDGYNVCIFAYGQTGAG
KSYTMMGRQEEQQEGIIPMICKDLFTKIQDTETDDLKYSVEVSYMEIYCERVRDLLNP
GEHLOVGKEETFRYIVLOANGGIGAEYADIFCOFNFLHRHEEAFSTEPVKNSASGAPLG
FYHVONITVPVTKSFIEYLKTOPIMFKIFGHYQTHPLHKDAGFYPSTPHEHSDDLPGF
IPISOPVRSPKFGPLDCAPTSTVLAKHDVLVWFEICELAPDAGBYVPSVVFHSUDLFG
GLFLLHQGIQRRIRITIVHEPTTEVKWKDINELVVGRIRNTPESSDEQDEDACVLSLG
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Query Match
Best Local Similarity
Matches 1036; Conserv

Conservative

0;

Score 437; DB 10; Pred. No. 3.8e-113; 0; Mismatches 725;

Length Indels

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Faculty of Medicine, Department of Anatomy an
Hongo, Bunkyo-ku, Tokyo 113, Japan
(E-mail:yamazaki@kinesin.kaibol.m.u-tokyo.ac.
Tel:3-3812-2111(ex.3336), Fax:3-5689-4856)
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The neuron-specific kinesin superfamily protein KIF1A is a unique
monomeric motor for anterograde axonal transport of synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinesin family protein KIFla; monomeric motor; neuron-specific kinesin superfamily motor; axonal transport; organelle transport Mus musculus Brain cDNA to mRNA.

Mus musculus
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ETPKSFSEDYSYMSHTSSEDINYASOKOVYRDJGEEMLOHAFEGYNVCIFAYGOTGAG
KSYTMMGKQEKDOQGIIPQLCEDLFSRINDTINDMSYSVEVSYMEIYCERVRDLLNP
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AVFNIIFTOKKHDAETHITTEKYSKISIDDIAGSERADSTGAKGTRIKEGANINKSIT
TIGKVISALAEMDSGPNKNKKKKKDEIPIPYRDSYLTMLLRENLGGNSRTAMVAALSPA
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DIMTNALVGMSPSSSLSALSSRAASVSSLHERLIFAPGSEEALIRLKETEKIIIRLDLLYAGGLGDIT
DIMTNALVGMSPSSSLSALSSRAASVSSLHERLIFAPGSEEALIRLKETEKIIIRLDLLYAGGLGDIT
DWSKRTTAMVAALSPA
DINYDETISTLRYAADRAKOIRCNAIINEDDNIKLIRELKDEYTHLINEDLLYAGGLGDIT
DWSKKTTEALIREMEDRIADELEDOYREREREBATYLLDOORLDYESKLEALGKOMDSRY
VISKKVIEPSILRSGNRIIMGKSHVFRENHPEQARGERERTPCAETPAEPVDWAFAQR
ELLEKOGIDMKQEMERBALDOYREREREBATYLLDOORLDYESKLEALGKOMDSRY
YPEVNEEEEEPEDEVOWTERECELALMAFRKWKWYQFTSLRDLLMGNAIFLKEADAIS
VELKKKVGFGFVLLTDTLYSPLEPDLLPPEAAKDRETREPRTIVAVEVQDQKKGATH
YWTLEKLRQRLDLMREMYDRAAEVPSSVVEDCDUNVTIGGDPFYDFEFWFFLUGRAFVY
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DOHFEKFOSESCEVGMSRSGTSQEELAIVEGGGGADAGESADEVNNNTCSAVPPEG
LMDSPEKRAALDGPLDTALDHLALGSFTFFTRVTVLAETGGHTRWEEVERLVYGRIFHRHDE
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TDEALIDPNILSLNILSSGYVHPAQDDRVFFGNDTRTFYQFEAAMDSSMHNSLLLNRV
TPYREKIYMTLSAYIERSGFGSGFGMORRRRYLDTSVAVVRGEENLAGAFRSGSSLRA
TEGGNFSPLSKEVAPATKLSTMTRESGGFCKLBANGSGSSCASS
LSABEGOPSDLEALNUCTUPAJ ITKDFCMVTYSRDAKLPAGGRSKLSEMSVTLM
LSABEGOPSDLEALNUCTUPAJ TIKDFCMVTYSRDAKLPAGGRSKLSEMSVTLM
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LSABEGOPSDLEALNUCTUPAJ TIKDFCMVTYSRDAKLPAGGRSLASERSSGASSP
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LSABEGOPSDLAALTHENTERSTCTSLILERKGATTORPGPEVLSPAARSESDLILLSAKKTD
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MYNSDKDTVERFVLNLSTAQVEYSEDQQAMLKTPNTFAVCTEHRGILLQANSDKDMHD
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/protein_id="BAA06221.1"
/db_xref="GI:976235"
                                                                 WLYAFNPLLAGTIRSKLSRRRSAQMRV"
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etazoa; Chordata; Craniata; Vertebra theria; Rodentia; Sciurognathi; Muri	Mus musculu Eukaryota; Mammalia; E	ORGANISM	
GI:4512329 (Strain:ICR mouse) 4 weeks cDNA to mRNA.	AB0 KIF Mus	SION WORDS RCE	VER KEY SOU
5739 bp mRNA linear ROD 24-FEB-19mRNA for KIF1B-beta, complete cds.	AB023656  N Mus musculus AB023656	RESULT 4 AB023656 LOCUS DEFINITION ACCESSION	ABO LOC DEF
AACCACCCTGA	CACGTGTTCCGG	1887	DЪ
.ttcaaccatccggaagaagctcgtgcggaacg 1802	atttttcga	1758	Qy
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CAGCGAGGAGGCTATTGAAAGGCTGAAGGAAACAGAGAAGATCATTGCTGAACTCAATGA 1466	CAGCGAGGAGGCTA	1407	망
tygaycaactyaaccagagtyagaagctctatcgggatctcaatca 1358	caaggcagaaatcg	1299	Qy
CTGTCCAGCCGTGCAGCCTCTGTGTCCAGTCTCCATGAGCGCATCTTGTTTGCTCCAGG 1406	CCTGTCCAGCCGTC	1347	₽
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caggacatgttccggcgtattaatgaactgcagaaggacaagaacctcacttgcaccgtc 456
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TIGKVISALAEVSKKKKTDE IPYROSVLTWILIRENLGGNESRTAMVAALSPADINVDE
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TILSTLRYADRAKQIKCNAVINEDPNAKUTRELKEEVITRIKDILTRAGGIGDI IDTSMGS
LTSSDSSCSLINSQVGLTSVTSIQERINSTPGGEBAIERUKESEKI IAELNETWEEKLR
KTEAIRMEREALLAENGVAIREDGGTLGVESPKTPHLVNLNEDPLMSSCLLTYIKDG
ITRVGQADAERRODIVLSGAHIKEEHCLFRSERSNTGEVIVTLEPCERSETYVNGKRV
AHPVOLRSGNRIIMGKNHVFRENDEDARAEREKTPSAETPSEVDWTEAQRELLEKQ
GIDNKQEMERRLOEMELLYKKEKEEADLLLEQORLDVESKLOALOROVETRSLAAETT
EEEEEEEEVPWTQHEFELAOMAFRKWKOHQTSILDLLMGNAVYIKEANAISVELKK
VOFQFVLLTDDILYSPVPPLLDSEMEKTHEDRPFPTVVAVEVODLKNOATHYWSIDK
LKQRILDLMREMYDRAGEVASSAODDSETTMTGSDFYDRFHWRKLVGSSPIFHGCVNE
RLADRTSSPTFSTADSDITELADEQORAMEDFDDEAFVDDTGSDAGTEEGSELFSDGH
DPFIDNSENWFILVGRAFVYLSHLLYFVPLIHRVAIVSEKGEVRGFLRVAVOAIAADEE
APDYGSGIRQSGTAKISFDNEYENQSDESSAMTRSGLSLEELRIVEGQGQSSEVISP
PEEVNRNNDLOLKSGTLLDKMYMEGFSEEIGNHIKLLGSAFTFRVTVLDASGILPEYA
DIFQORPLHHUBAEFSTEPLKINGRGGFSEEIGNHIKLLGSAFTFRVTVLDASGILPEYA
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ASSPCQEFEOFQI VPTWETPYLIARAGKNEFILNLYDDLEEVRAGSVVSKKGYLHFKEPL
SSWMAKHFVVVRRPYVFI YNSDKDPVERG I INLSTAQVEY SEDQQAMVKTPNTFAVCT
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EAPKSFSFDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAG
KSYTWMGKQEESQAGIIPQLCEELFEKINDNCNEEMSYSVEVSYMEIYCERVRDLLNP
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cactccaaagaaatgccacatctagtcaacttgagcgatgatcctcttctggctgagtgt 1	CCTTGTTGGCTGAGATGGGAGTTGCCATACGGGAAGATGGGGGGACACT	gcggcgctcgaggagctgggtatcagcatcgaaaagggctttgttggcccttac 1	ctcaatcagacctgggaagagaagctggccaagaccgaggaaatccacaaggaacgagaa 1	aaaatgagcaaggcagaaatcgtggagcaactgaaccagagtgagaagctctatcgggat 1	cccgacacgccgctcgagaagcaaatcgtgtcgattcagcagccggatgcgacagtcaag 1	agtggtggaggtggaggtggtgcaggaggttctggcgggccagtggaggaatcgtacccg 1	atgatccgcgagttgaaggaagtactcgcgcagctgaggagcaaactccagagc 1	gcggactctgcgaagcgaatcaagaaccacgcagtggtcaatgaagacccgaacgcgcgg l 	attgccgccatttcgcctgctgatattaactttgaagagactctcagtacccttcgatat 1	gattoggtactgacgtggcttctgaaggactccttgggaggcaactcgatgacgccatg 9	gcagcgctagcggatatgtcgtcgggaaaacagaagaagaatcagttagtaccttaccga 93 	gcgcgactgaaggaggtgcagagatcaaccgctcactttcgaccctaggtcgtgtgatt 8	aagatcagtctggtagatttggcgggttctgagcgagcaacgtccaccggagctactgga	ttgaccttgacgcaaaagtggcatgatgaagagaccaaaatggacacagagaaggttgcg 7:	agaacggttgccgccacaaacatgaacgagacatccagtcgatcccacgccgtcttcact 69	aagctggtcgtcgatcattccaagaaatcgaaaatctcatggatgagggcaacaaagcc         6.	aaggggaatctcaaggtccgagaacacccgtcgaccggcccctacgtggaggacttggcg 57	gaagtttcgtacttggaaatttacaatgaacgagtgcgagacttgctgaatccgtcgaca 51 	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-SEP-1993) Masaomi Nangaku, University Anatomy and Cell Biology; 7-3-1 Hongo, Bunkyo-ku, To (Tel:03-3812-2111(ex.3336), Fax:03-5689-4856) 2 (bases 1 to 4862) 2 (bases 1 to 4862) Nangaku, M., Sato-Yoshitake, R., Okada, Y., Noda, Y., Ta Yamazaki, H. and Hirokawa, N. KIFIB, a novel microtubule plus end-directed monomer protein for transport of mitochondria cell 79 (7), 1209-1220 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nomura, N., Nagase, T., Miyajima, N., Sazuka, T., Tanaka, A., Seki, N., Kawarabayasi, Y., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0041-KIAA0080) analysis of cDNA clones from human cell line KG-1 DNA Res. 1 (5), 223-229 (1994)
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                                       /translation="MSGASVKVAVRVRPPNSRETSKESKCIIQMQGNSTSIINPKNPK
EAPKSPSFDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAG
KSYTMMGKQEESQAVIIPQLCEELFEKINDNCNEEMSYSVEVSYMEIYCERVRDLLNP
KNKGNLRVREHPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNNNETSSRSH
AVFTIVFTQKKQDPETNLSTEKYSKISLVDLAGSERADSTGAKCTRLKEGANINKST
TLGKVISALAEVSKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDE
TLSTLRYADRAKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDTSMGS
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
293. .3745
LTSSPSSCSLNSQVGLTSVTSIQERIMSTPGGEEAIERLKESEKIIAELNETWEEKLR
KTEAIRMEREALLAEMGVAIREDRGDIGVFSPKKTPHLVNLNEDPLMSECLLYYIKDG
                                                                                                                                                                                                          /protein_id="BAA04503.1"
/db_xref="GI:407339"
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GDEKIEDMMYTGKGGTDVDDLKVHIDKLEDILGEVKKONNMKDEEIKVLRNKMLKMEK
VLPLIGSOEDKSOGSHKTKEPLVAGANSYSDNOYSKGESGELGKEERVSQLMNGDPAF
RRGRLRMMRODGIRFKKLLQOEDKYGLRGNVDHRFIPPENKKPRFPFKSNPHOHNOW
SPGTHIITEDEVIELRIPKDEEGKEMKEESOEKVGRAASRDVOSANGTRSODHJOV
SKQHISNOOPPPOLRWRSNSLNNGOPKTTRCQATASSESLNSHSGHPTADLQTFOAKR
HIHOHROPYCNYNTGGQVEGSTASCCQKQTDKPSHCNQFVTPPRMRRQFSAPNLKAGR AHPVQLRSGNRIIMGKNHVFRFNHPEQARAEREKTPSABTPSEPVDWTFAQRELLEKQ GIDMKQEMEKRLØEMEILYKEKEEADLLLEQQRLDADSDSGDKDSDKRSCEESWKLIT SLREKLPSKLOTIVKKGCLPSSGKKREPIKMYQIPQRRRLSKDSKWYTISDLKIQAL KEICYEVALNDFRHSRQEIEALAIVKMKELCAMYGKKDPNERDSWRAVARDVWDTVGV ITRYGQADAERRODIVLSGAHIKEEHCLFRSERSNTGEVIVTLEPCERSETYVNGKRV

polyA\_signal BASE COUNT 1435 & ORIGIN 4847. .4852 1064 c 1200 g 1163

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Length 4862;

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                      gcagcgctagcggatatgtcgtcgggaaaaacagaagaagaatcagttagtaccttaccga
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Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                    GI:15212239
 Chordata;
Primates;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                       PRI 18-AUG-2001
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TCACCCGAAGATCCCTGTTTTGCATCTCAGAACCGTGTGTACAATGACATTGGCAAGGAA
                        ---aagaatgctcccaactatgcgagacaggaagacctattccaagatctcggagtcccg
                                                                                AAGAATCCAAAGGAAGCTCCAAAGTCCTTCAGCTTCGACTATTCCTACTGGTCTCATACC 184
                                                                                                         aaaactattatggatggcccgaaggcatttgcgttcgatcggtcgtattggtcctttgac 216
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Submitted (03-JUL-2001) Biological
Wonchon-dong Paldal-Gu, Suwon, Kyeo
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Park, M., Shin, H., Lee, Y.M.,
Identification of the human
superfamily motor protein
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k,M., Shin,H., Lee,Y.M.,
                                                                                                                                                                     Conservative
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EAPKSFSFDYSYMSHTSPEDPCFASQNRYYNDIGKEMLLHAFEGYNVCLFAYGOTGAG
KSYTMMGKQEESQAGIIPQLCEELFETINDNCNEEMSYSVEVSYMEIYCERVRDLLNP
KNKGNLRVRDHFLRGPYVEDLSKLAVTSYTDIADLMDAGNKARTYNAATNNNETSSRSH
VVYTIYFQKKHIDNETILATVKYSKTSLVDLAGSDRAASTGAKGTRLKEGAIINKSLT
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TLSTLRXADRAKQIKCNAVINEDPNAKLVRELKEEVTHLADLLRAGGLGDIIDTSMGS
LTSSPSSGLSGQVGLTSVTSTOERINGTPGGEBAIERLKEESEKIIAELMETWEEKLR
KTEAIIMEREALLAEMGYAIREDGGTLGYFSPKKTPHLVNLNEDPLMSECLLYYIKDG
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GIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDADSDSDKRSCEESWKLIT
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KEICYEVALNDFRHSRGEIEALAIVKMELCAMYGKDDWGRRDSWRAVARDVWDTVGV
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KEICYEVALNDFRHSRGEIEALAIVKMELCAMYGKODWGELAKEERVSQLMNGDPAF
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VLPLIGSGENSGSGKARSPTKOLRRQNVPHREIPPENRKDEFPKSNPKHRMLKMEK
VLPLIGSGENSGSGKARSPTKOLRRQNVPHREIPPENRKDEFPKSNPKHRMSW
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GEGERLEWMRODGOIRFKNLOOGLITKOLRRQNVPHREIPPENRKDEFPKSNPKHRMSW
                                                                                                                                                                                                                                                                                              /gene="KIF1B"
/note="Region: mo
1502. 1750
/gene="KIF1B"
/note="Region: FH
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35. .1120
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26. .1072
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IQVSKQHINNQQQPPQLRWRSNSLNNGQPKSTRCQASASAESLNSHSGHPTADVQTFQ
AKRHIHQHRQSYCNYNTGGQLEGNAATSYQKQTDKPSHCSQFVTPPRMRRQFSAPNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to mouse KIF1B; similar to KIA/KIAA1448 sequences found in GenBank Accession AB011163 and AB040881, respectively"
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/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.22"
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Pred. No. 4e-102;
0; Mismatches 696;
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Kyeongki-do
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Yang, H.W., Takita, J., Chen, Y.Z., Soeda, E., Plao, H.Y., Hashizume, K
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WATMADLKMQAVKEICYEVALADFRHGRAEIEALALKMRELCRTYGKPDGPGDAWRA
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ELQALKDRMLAMERVIPLAQDHEDENEBGGEVPWAPPGGSEAAEBAAPSDRMPSARPP
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Submitted (26-MAY-1998) Osamu Ohara, Kazusa DNA Research
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chib
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-43
                                                                       Ohara,O.,
                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                         Ishikawa, K., Nagase, T., Suyama, M., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O. Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 5 (3), 169-176 (1998)
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AVFTIVFTQRCHDQLTGLDSEKVSKISLVDLAGSERADSGARGMRLKEGANINKSLT
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EEGSVRGALPAVSSPPAPVSPSSFTTHNGELEPSFSPNTESQIGPEEAMERLQETEKI
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ETYVNGKLYTEPLYLKSGNRIVMGKNHVFRENHPEQARLERERGVPPPDGCPSEPVDW
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RSCEESWRLISSLREQLPFTVGTIVKRGKHPSSKRAETEXLAEKTVQJIPGRRRLQGKDP
RATMADLKKNQAVKEICYEVALADFRHGRAEIEALAALKHRELCRTYGKPDGPGDAWRA
VARDVWDTVGEEEGGGAGSGGGSEEGARGAEVEDLRAHIDKLTGIIQEVKLQNSSKDR
ELQALRDRALRMERVIPLAQDHEDENEEGGEVPWAPPEGSEAAEEAABEAAFRAPSDRARPSSRARP
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/clone_lib="pBluescriptII
/dev_stage="adult"
368. .3679
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HDCKLRFPFKSNPQHRESWPGMGSGEAPTPLQPPEEVTPHPATPARRPPSPRRSHHPR
RNSLDGGGRSRGAGSAQPEPQHFQPKKHNSYPQPPQPYPAQRPPGPRYPPYTTPPRMR
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DAPKSFTFDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAG
KSYYMMGRQEPGQQGIVPQLCEDLFSRVSENQSAQLSYSVEVSYMEIYCERVRDLLNP
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/db_xref="GI:3327226"
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Sciences, University of
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Nakajima,K. and Hirokawa,N.

Direct Submission

Submitted (08-NOV-2001) Kazuo Nakajima, University of Tokyo,
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Tokyo 113-0033, Japan (E-mail:kazuo@m.u-tokyo.ac.jp,
Tel:81-3-5841-3336, Fax:81-3-5689-4856)
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Molecular Motor KIFIC Is Not Essential for Mouse Survival Motor-Dependent Retrograde Golgi Apparatus-to-Endoplasmic Transport
Mol. Cell. Biol. 22 (3), 866-873 (2002)
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Caenorhabditis elegans (strain N2) cl
Caenorhabditis elegans
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Rhabditoidea; Rhabditidae; Peloderinae;
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C. elegans unc-104 gene encodes a
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                                                                                                                       /gene="unc-104"
111. .4865
                                                                                                                                                                                                                                                          Location/Qualifiers
              /product="kinesin-related protein"
/protein_id="AAA03517.1"
/db_xref="GI:156478"
                                                                       /gene="unc-104"
/standard_name="uncoordinated-104"
/note="putative; putative"
                                                                                                                                                                                                          /organism="Caenorhabditis
/db_xref="taxon:6239"
translation="MSSVKVAVRVRPFNQREISNTSKCVLQVNGNTTTINGHSINKEN/
                                                             /codon_start=1
                                                                                                                                                                                /partial
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HKKGPKLPAHVHÖLEKLQESEKLMAEIGKTWEQKLIHTEEIRKOREEELRDMGLACA
EDGTTLGVFSPKKLPHLVNLNEDPLNSECLIYYLKEGVTSVGREEAEHRPDILLSGEA
ILELHGET NEDGNYTLTHKRUNASCYINGKOVTTPTULHTGSRVLIGBHLVERKYSGEA
ILELHGET NEDGNYTLTHKRUNASCYINGKOVTTPTULHTGSRVLIGBHLVERKYSGEA
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IKNSKTFLHYLHHFPIIFEVPGHFQPKSEQFNFERQNSALGRRLSTKLTFQQPSLVIS
TPVKSKKANAPIQNNASSYKSKHDLLVNFEICELANNGEYVPTIVDHAQGLPTHGIFL
LHQGIQRTRITTICHEKGELKWXDCQELVVGRITAGAFBWAGGDDVDULSIGLFPGGFFM
EFSMDDRTFFQFEAAMDSSLINSPLNRVSNYGDDIYMTLSAYMELDGCAQPAVYKD
LESMDDRTFFQFEAAMDSSLINSPLNRVSNYGDDIYMTLSAYMELDGCAQPAVYKD DRDLVIRGIINLANARIEHSEDQQAMVKVPNTFSVCTNQRGFIMQMMPGDEMYDWLYA INPLMAGQMKLHGNQNGTTLKSPTSSSSIAAS"
1 918 c 1064 g 1436 t LCLLIYARDSKISAASRFCRSLYGGISKSPEMNRYPGYYQLCLKDGSDSGSPGAIRRQ RRYLDTSSAYYRGEENLGQWRPRGDSLIFEHQWELEKLTRLQQYERYRLFLRLRDRLK GKKNKGEARTPYSPCDPYCAIPESIKLDEKDKGIYGKYLGLIRRKIPMNKDPPTGNKA GNLRVREHPLLGPYVDDLTKMAVCSYHDICNLMDEGNKARTVAATNMNSTSSRSHAVF FSFNFDHSYWSFARNDPHFITQKQVYEELGVEMLEHAFEGYNVCIFAYGQTGSGKSYT MMGKANDPDEMGIIPRLCNDLFARIDNNNDKDVQYSVEVSYMEIYCERVKDLLNPNSG QELSDESGSNSITSPVSDKSLIKSSRSSDLLCRQKSKSDQNLASNDDIVDNLGGMKRS LSTLRYADRAKQIVCQAVVNEDPNAKLIRELNEEVIKLRHILKDKGIDVTDVQETPGK LVISKLAEESTKKKKSNKGVIPYRDSVLTWLLRENLGGNSKTAMLAALSPADINFDET TIVLTQKRHCADSNLDTEKHSKISLVDLAGSERANSTGAEGQRLKEGANINKSLTTI LSGSRILQLNILVÞEVLEERVGVVVSKKGYMNFLEEKTQGWTRRWVIVRRPYILLFRD

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gagacatccagtcgatccccacgccgtcttcactttgaccttgacgcaaaagtggcatgat
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54.8%;
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Pred. No. 7.1e-89;
0; Mismatches 680
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                                                                                       AATGCATCTTGCTATATAAATGGAAAACAAGTGACAACTCCTACTGTATTACACACAGGA
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KIERKQPKTFAPDHCFYSLNPEDENFASQETVEDCVGRGILDNAFGGYNACIFAYGQT
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SQQLINKLTGJMREMYGBAMESLLANGGBPATSKLLGARNDTLHEEPLAGGBPISHRSDEPBSYSDS
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LATLSMSSTSSGYGGAVSCNNLSNEDIASMRSMSIDETPDPDRVNSNSPNRQARV
NRPLKDMRAKLGBPHVORDRSOMHSSDEADTSTHLEGDLSRRSDELSHKSPDLLERBKKTURE

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/db_xref="taxon:7227"
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ELPAGKVVRRKKSNTQPPSNGNSINNNNNGTTQVPRINHRASVAKMEGLAAYLDSSIM
TSSTEVDEESKDVELVLPEWLVVGESVLIRPYNTSGVIRFVGTTEFQPGAWIGVELDT
                                                                                       PTGKNDGSVKGVQYFQCKPKHGMFVRSDKLMLDKRGKAMRAYKAAEKSNSISKEMSTS
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Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                           CATCGATAACCTCATGACCGAAGGCAACAAGTCACGAACGGTGGCCGCCACCAATATGAA
                                                                                                                                                                                                                                                                                                                                                                                              ATCCACACCCGAG----CTTATGTACAAGGTGGAGGTGTCCTACATGGAGATCTATAACGA
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                           GAAAGACAATTTGGGTGGCAATTCCAGAACTGTTATGGTAGCGACAATCTCGCCATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-FEB-2000) Terunaga Nakagawa, Graduate School Medicine, University of Tokyo, Department of Cell Biology & Anatomy; 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:terunaga@m.u-tokyo.ac.jp, Tel:81-3-5841-3336,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Novel Motor, KIF13A, Transports Mannose-6-Phosphate Receptor to Plasma Membrane through Direct Interaction with AP-1 Complex Cell 103 (4), 569-581 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus mRNA
AB037923
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Nakagawa, T. and Hirc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax:81-3-5689-4856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa, T.,
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/strain="ICR"
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accggcccctacgtggaggacttggcgaagctggtcgtgcgatcattccaagaaatcgaa
                                                                                                                                                                                                                                                                                                                                       cgagacttgctgaatcc---gtcgacaaaggggaatctcaaggtccgagaacacccgtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catggcgtgatcccgcggatttgccaggacatgttccggcgtattaatgaactgcagaag
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accaaaatggacacagagaaggttgcgaagatcagtctggtagattttggcgggttctgag
                                                                                   tccagtcgatcccacgccgtcttcactttgaccttgacgcaaaagtggcatgatgaagag
                                                                                                                                             aatotoatggatgagggcaacaaagccagaacggttgccgccacaaacatgaacgagaca
                                                                                                                                                                                                                                CTGGGGCCGTATGTCGATGGTCTCTCAGCTGGCTGTCACCAGCTTTGAGGACATTGAG
                                                                                                                                                                                                                                                                                                                     CGGGACCTCTTGGACCCCAAAGGGAGCAGGCAGTCTCTGAAAGTCCGAGAGCATAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCTTATCCCAAGGCTCTGCTGTGCTCTGTTTCAAAGGAT---CGCCCTGGAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ttcgcctacggtcagaccggttcgggcaagtcctattcaatgatgggctatggcaaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCAAGTGCCTCGGGGAAGGAATTCTCGAGAAAGCCTTTCAGGGATACAATGCTTGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTGCTTTTGGTCCATGGATGAATCGAACACAAATATGCTGGTCAAGAAGTCGTT
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                                                          AGCAGCCGTTCCCATGCGGTCTTCAACATCATCATCACACAGACGCTGTATGACCTACAG
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SGKDETLAVPLEENSALPKGTPSPQSIPEESSRAPCRTASCSELDVGFSKDGHQAREF
CPGEVTIEHTNILEDHSFTEFMGVSDGKDFDGLADCSVGEPSRRALTNETDHKGIP
ERPPDADRLHRKIENDQEATATR*
1708 c 1841 g 1357 t
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ALTVSPFKAFSPQPPKFFKPLMPVKEEHKKRLALEARPLLSQEDSEEEENELEALSRK
LMLTQPYVPVEFADFSVYNASLENREWSSSKADLTDSRALEKAVSRSPTTSSLTSGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIKRREYLDEQIKKYSNKKEKTEDDMEREARLVEQWYGLTŒERNAVLYPAPGSGIPGA
PADWYPPGMETHIPYLFLDLNADDLSANEQLYGPHASGYNSTLPKEHGSQFFYLPII
KHSDDEVSATASWDSSYHDSLHLNRYTPQNERIYLIVKTYVQLSHPAAMELVLRKRIB
ANIYNKQSFYGSLKRRLSLINICYSCGYTYEIYSNIFKATEEIEDRETLALLAARSEN
EGTLDGETYIEKYTRGYLQVENILSLERLRQAVTYKEALSTKARHIRRSLSTPNVHNY
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59.5%;
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Pred. No. 2.6e-87;
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HSA291578
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaagagactctcagtacccttcgatatgcggactctgcgaagcgaatcaagaaccacgca 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttgggaggcaactcgatgaccgccatttgccgccattttcgcctgctgatattaacttt 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagaagaatcagttagtaccttaccgagattcggtactgacgtggcttctgaaggactcc 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (24-OCT-2000) Jamain S., I
Strue du Docteur Roux, 75724 Paris
Location/Qualifiers
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Jamain, S., Quach, H., Fellous, M. and Bourgeron, T. Identification of the human KINESIN-13A gene, homologous Drosophila kinesin-73 and candidate for schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSA291578 5700 bp
Homo sapiens mRNA for KINESIN-13A1
AJ291578 GI:12054029
KIN13A gene; KINESIN-13A1.
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LDPKGSFSNMGHAEOLGLI PRLCCALFKRISLEQNESQTFKVEWSYMEIYNEESSNIN
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KEKLEESEKLIKELTVTWEEKLRKTEEIAQERQRQLESMGISLEMSGIKVGDDKCYLV
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BASE COUNT ORIGIN

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Search completed: July 25, 2002, 05:37:18 Job time: 6591 sec

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                                                        Thermomyces lanugi Drosophila melanog Human polynucleoti Human polynucleoti Human KLIMP CDNA.
                                                                                                                                                                                                      Description
Drosophila melanog
Human diagnostic a
Human kinesin-like
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$\vdash$	AAD23971	24	12	4.0	95	45	
	AAC42969	21	4989	4.1	•	44	
Arabidopsis thalia	AAC46311	21	4557	4.1		43	
Human bone marrow	AAH89871	22	1391	4.2	98.2	42	
DNA encoding novel	AAS84836	23	4550	4.2	9	41	
Human polynucleoti	AA181860	22	520	4.2	99.6	40	ი
Human polynucleoti	AAI58253	22	8503	4.3	100.4	39	
DNA encoding novel	AAS70692	23	8083	4.3	100.4	38	
cDNA encoding nove	AAS45225	22	5607	4.4	102.6	37	
	AAS96044	24	1053	4.4	103	36	
	AAV47580	19	1053	4.4	103	35	
	AAX26819	20	9626	4.4	104	34	
	AAH05392	22	814	4.4	104.6	33	
phila	ABL13337	23	3720	4.5	106.2	32	
cDNA seq	AAH15830	22	1950	4.5	106.2	31	
cervical	AAH72653	22	4790	4.5	106.4	30	
kinesin	AAD23970	24	4757	4.5	106.4	29	
Ħ	AAD23972	24	1230	4.5	106.4	28	
Drosophila kinesin	AAV67162	19	3572	4.6	107.8	27	
Drosophila melanog	ABL09774	23	8848	4.7	110.4	26	a
a	AAF97834	22	5368	4.7	110.6	25	
	ABA83095	22	5368	4.7	110.6	24	
	AAS45037	22	5884	4.8	112	23	
ucleotide	AAS99916	24	2111		114.8	22	
secreted	AAC02955	21	459		118.6	21	
nervous	ABA17294	22	1407	5.3	124	20	
co.	AAL23900	22	758		124.4	19	a
	ABL14182	23	12075		134.8	18	
	ABL12290	23	16532		161	17	
	ABL16732	23	4034	•	164.4	16	
	ABL16733	23	2034	7.0	164.4	15	
Leishmania chagasi	AAT42166	17	3319		177.8	14	
K39 gene of Leishm	AAQ70152	15	31		٠	13	
phila melanc	ABL09775	23	52		276.8	12	
diagnosti	030	22	2248	11.9	٠	11	
Human secreted pro	AAF22377	21	70	13.1	309	10	

ALIGNMENTS

Thermomyces lanuginosus kinesin motor protein TL-gamma DNA.

26-OCT-1999 AAX87656;

(first entry)

RESULT AAX87656

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AAX87656 standard; DNA; 2352

ВР

WPI; 1999-493950/41. P-PSDB; AAY06618. neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; ss. TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; Goldstein LSB, (REGC ) UNIV CALIFORNIA. 23-JAN-1998; 22-JAN-1999; W09937659-A1. Thermomyces lanuginosus. 29-JUL-1999. 98US-0072361 99WO-US01355 Sakowicz æ

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Query Match
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Matches 2352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and containing a polypeptide or polynucleotide of the invention may be used to treat diseases, peripheral neuropathy and containing a polypeptide or polynucleotide containing a polypeptide or polynucleotide contains, such as peripheral nervous injuries, peripheral neuropathy and containing the system disease, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic contains and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assaws for receptor activity, arthritis and inflammation, leukaemias and

Claim

1; SEQ ID NO 1393;

as

nucleic acids and as central nervous

polypeptides, useful
system injuries -10078pp; English.

for

treating disorders

2001-442253/47 DB; AAM40034.

C.N.S Note:

The sequence data for this patent did

not

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03-AUG-2000;
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Homo sapiens.

WO200153312-A1

26-JUL-2001

26-DEC-2000; 2000WO-US34263

21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000US-0653450.

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P-PSDB; AAY51328.

Nucleic acid sequences encoding a human kinesin-like motor protein (KLIMP) useful for the treatment of diseases associated with inappropriate KLIMP expression such as cancers, neurological disorders and disorders of vesicular transport.

Claim 6; Fig 1A-J; 38pp; English.

This invention describes a novel human kinesin-like motor protein

(KIIMP) (1) which has cytostatic, anti-Convulsant, anti-Alzahmer's,

(KIIMP) (1) which has cytostatic, anti-Convulsant, anti-Alzahmer's,

anti-Parkinsonian, antidiabetic, anti-ulcerative, immunomodulatory,

antilnflammatory, anti-AIDS, antirheumatic and antiarthritic activity.

(1) and the protein it encodes may be used in the prevention, treatment
and diagnosis of diseases associated with inappropriate KLIMP expression
such as cancers, neurological disorders and disorders of vesicular
transport. For example, (1) (and vectors containing (1) (Iv)) and the

KLIMP polypeptide may be used to treat disorders associated with
decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and
cancers of the breast lung and prostate), neurological disorders (e.g.
epilepsy, Alzheimer's disease and Parkinson's disease), disorders of of
vesicular transport (e.g. diabetes mellitus/insipidus, Grave's disease
and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g.
cacquired immune deficiency syndrome AIDS), rheumatoid arthritis and toxic
shock syndrome). This sequence encodes the human KLIMP protein described
in the method of the invention.

Sequence 3930 BP; 872 A; 1111 C; 1266 G; 681 T; 0 other;

10; 286 346 cogtggcgcaaaatgtattgtgcggatggaaggaaatcaaaccatcctcacccctcctcc 125 302 359 406 416 466 643 80 ggctggtgcctcggtgaaagtggcagtgagggttcggccctttaacgcccgtgagaccag 139 Gaps gggcggtggaaatatcaaggtggtggtgcgggtacgcccgttcaacgcccgagaaatcga 65 caattgtatcttcgcctacggtcagaccggttcgggcaagtcctattcaatgatggg--agaacacccgtcgaccggcccctacgtggaggacttggcgaagctggtcgtgcgatcatt ---ctatggcaaggagcatggcgtgatcccgcgggatttgccaggacatgttccggcgtat acaggagccaggagaggagcatcgtgccccagctctgtgaggacctcttctctcgcgt taatgaactgcagaaggacaagaacctcacttgcaccgtcgaagtttcgtacttggaaat tgcgttcgatcggtcgtattggtc---ctttgacaagaatgctcccaactatgcgagaca ggaagacctattccaagatctcggagtcccgcttctggataatgcattcaagggttataa cgtgtgcatctttgcctatgggcagaccgggggctgggaaatcctataccatgatggggcg ttacaatgaacgagtgcgagacttgctgaatccgtcgacaaaggggaatctcaaggtccg 66 Length 3930; Indels Score 380.6; DB 21; Pred. No. 2.2e-103; 0; Mismatches 739; I Query Match Best Local Similarity 55.0%; Matches 1023; Conservative 9 198 99 186 287 303 360 584 243 347 407 417 467 477 524 윱 셤 ð ò ò 셤 ç a ç a ö g õ a ò a ô g ò

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The present sequence is human kinesin-like motor protein (KLIMP) cDNA from Incyte clone 1281811 obtained from colon cDNA library (COLNNOT16). KLIMP and the corresponding polynucleotide are useful for diagnosis, treatment and prevention of disorders associated with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland), neurological disorders (such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, peripheral nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; ischaemic cerebrovascular disease; stroke; Alzheimer's disease; bick's disease; luntington's disease; dementia; Parkinson's disease; vesicular transport disorder; cystic fibrosis; diabetes mellitus; AIDS; Acquired Immune Deficiency Syndrome; microbial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences encoding a human kinesin-like motor protein (KLIMP) useful for the prevention and treatment of diseases associated with inappropriate KLIMP expression such as cancers and neurological
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from brosophila and for elucidating cell signalling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 31355
                                               developmental biology; cell signalling; insecticide;
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Best Local Similarity 59.2%; Pred. No. 1.2e-94;
Matches 689; Conservative 0; Mismatches 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell proliferative disorder; Crohn's disease; lymphoma; leukaem acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human diagnostic and therapeutic polynucleotide (DITHP) #155.
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DTHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DTHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, [crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DTHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL; Liu TF, Roseberry AM, Rosen BH, Russor FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
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Dufour GE, Flores V, Fr
Liu TF, Roseberry AM, 1
Wright RJ, Yap PE, Yu.
Cohen HJ, Hodgson DM, 1
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its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AASJ0966-AASJ1196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention.
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                                                                                                                                                                                                            27;
                                                                                                                                                                                   Length 2275;
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                                                                                                                                                Sequence 2275 BP; 697 A; 479 C; 597 G; 502 T; 0 other;
                                                                                                                                                                                   Score 321; DB 22;
Pred. No. 1.4e-85;
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58.1%;
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The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFIA and KIFIB proteins. The sequences disolosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used
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                                                                                                                                                     cttctgaaqgactccttgggaggcaactcgatgaccgccatgattgccgccatttcgcct 1014
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intracellular transport; neurological disorder; infertility;
biallelic marker; spontaneous abortion; neonatal chromosome disorder;
   866
                                                                                        954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides -
                              tcgtcgggaaaacagaagaagcagttagttaccttaccgagattcggtactgacgtgg
                                                                                                            Human kinesin-like protein HKLP coding sequence SEQ ID NO: 3.
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P-PSDB; AAB36227.
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                                                                    DB 21; Length 10682;
                          Sequence 10682 BP; 2817 A; 2443 C; 2602 G; 2812 T; 8 other;
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                                                                   Score 316.2; DB 21;
Pred. No. 8.9e-84;
1; Mismatches 389;
 in disease diagnosis and population studies.
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59.6%;
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Matches 616;
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AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134

to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
and polypeptides homologous to them. Human secreted proteins have
activities based on the tissues and cells the genes are expressed in.

Examples of activities include: immunosuppressive; antiarthritic;
antifhreumatic; antiproliferative; cytostatic; cardiant; vasciropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
cused to prevent, treat or ameliorate a medical condition in e.g. humans,
mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
also used in diagnosing a pathological condition or susceptibility to a
pathological condition. Disorders which are diagnosed or treated include
autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
disorders e.g. ordiac arrest, cerebroascular disorders e.g. cardiovascular
clischaemia, angiogeneals, nervous system disorders e.g. Alzheimer's
disorders e.g. cardiac arrest, cerebroascular disorders e.g. Alzheimer's
disorders e.g. cardiovascular cliverior en also be used to
aid wound healing and epithelial cell proliferation, to prevent skin
aging due to sunburn, to maintain organs before transplantation, for
                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; exerboprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; andiogenesis; nervous system disorder; crebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; food additive; preservative; ss.
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                         is.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                            AAF22377 standard; cDNA; 1701 BP
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20-JAN-2000; 2000US-0176931.
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supporting cell culture of primary tissues, to regenerate tissues and chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAP22364 to AAP22372 and AAB63133 represent sequences used in the exemplification the present invention.
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                                                                                                                                              28;
                                                                                                                      Length 1701;
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                                                                                 G; 390 T; 6 other;
                                                                                                                   Score 309; DB 21; ]
Pred. No. 4.7e-82; 5; Mismatches 465;
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Best Local Similarity
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Shah P, Chalup MS;
Panzer SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human diagnostic and therapeutic molecule; dithp; gene therapy; thalassemia; cardiovascular disorder; cell proliferative disorder; cancer; neurodegenerative disorder; intoimmune disorder; infectious disorder; cardiovascular disorder; cardiovascul
                                                                                                                                ctgotcaaagacagcctcggggggtaacagcaagmccgccatggtggctactgtgagtcct
tcgtcgggaaaacagaagaatcagttagtaccttaccgagattcggtactgacgtgg
                                                                                                                                                                               gctgatattaactttgaagagactctcagtacccttcgatatgcggactctgcgaagcga
                                             agtgctggcaaa---agcargaataaatttgttccatatcgtgactcagttctcacttgg
                                                                                       cttctgaaggactccttgggaggcaactcgatgaccgccatgattgccgccatttcgcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic (dithp) cDNA sequence #42.
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                                                                                                             BH,
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                                                                                                                                                                                                                                                                                                                                                                  gaggaactcgcgcagctgagg 1155
                                                                                                                                                                                                                                                                                                                                                                                                          1156 gaagaagttgagaaactccgg 1176
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990S - 0.156565
990S - 0.1565624
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24-NOV-1999;
24-NOV-1999;
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30-NOV-1999;
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24-SEP-1999;
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01-DEC-1999;
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                                                                                                                                                                                              The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #42 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 2387342dec) cencodes a cytoskeletal molecule. The dithp polynucleotides may be used to diagnose a condition disease or disorder associated with human molecules. They can be used to identify the presence of similar nucleic acids. Dithp polynucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to screen for molecules which bind to them and modulate their activity Dithp polynucleotides can be used for gene therapy of disorders such as severe combined immunodeficiency syndrome (SCID), cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX deficiencies, cardiovascular disorders e.g familial hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers, neurodegenerative disorders, and developmental disorders. The antibodies can be infectious disorders and developmental disorders.
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                                                   Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----gaggcactggggactcaggaagagaacggaccaagaccttcacctatgactttt
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Pred. No. 3.3e-73;
0; Mismatches 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to analyse protein expression levels.
                                                                                                                                                      Claim 1; Page 276-277; 299pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%;
Matches 642; Conservative
WPI; 2001-281607/29
                                                                                                      thalassemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more
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614 tcatggatgagggcaacaaagccagaacggttgccgccacaaacatgaacgagacatcca 673
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                           683 ttatggatgcgggcaatatcaaccggaccaccgcagcgactgggatgaacgacgtcagta
                                                       gtcgatcccacgccgtcttcactttgaccttgacgcaaaagtggcatgatgaagagacca
                                                                     aaatggacacagagaaggttgcgaagatcagtctggtagatttggcgggttctgagcgag
                                                                                                                              caacgiccaccggagciactggagcgcgactgaaggagggtgcagagatcaaccgcicac
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                                                                                                                                                                                                                                                                                                                                         tgaaggactccttgggaggcaactcgatgaccgccattgccgccatttcgcctgctg
                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 23807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                            tttcgacctaggtcgtgtgattgcagcgctagcggatatgtcgtcgggaa-----
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11-JUL-2000; 2000US-0614150.
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gococtacgtggaggacttggcgaagctggtcgtgcgatcattccaagaaatcgaaaatc 613

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01876) and the encoded proteins
 cell-cell
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                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                      23; Length 3525;
for elucidating cell signalling and
                                    NO 23807; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                   Score 276.8; DB 23; Length
Pred. No. 3.4e-72;
0; Mismatches 407; Indels
                                                                                                                                                                                                              Sequence 3525 BP; 896 A; 914 C; 1009 G; 706 T; 0 other;
                                                                                                                                                                                                                                                   11.8%;
57.7%;
 Drosophila and
                                                                                                                                                                                                                                                                             Matches 576; Conservative
                                                                                                                                                                                                                                                                Similarity
                                      SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
ggettetgaaggaeteettgggaggeaaetegatgacgeeatgattgeegeeatttege
                                                                                                                                                                    ctgctgatattaactttgaagagactctcagtaccttcgatatgcggactctgcgaagc
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chagas1; acidic ribosomal antigen; LCP0;

Leishmania chagasi K39 antigen

09-MAR-1997

AAT42166;

Location/Qualifiers 455..3319 /\*tag= a

WO9633414-A2

24-0CT-1996

Leishmania chagasi.

epitope; K39; ss.

Leishmania

96WO-US05472 95US-0428414

19-APR-1996; 21-APR-1995; (CORI-) CORIXA CORP.

Reed SG;

WPI; 1996-485884/48

P-PSDB; AAW03691

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gacctgcttgggaagcggaagaagggtgtgaagggcggcggcgaggaggtgtacgtggac 1069
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New Leishmania acidic ribosomal P-protein family poly:peptide - used to develop prods. for diagnosis, detection and protection against Leishmania infections

Disclosure; Page 43-48; 76pp; English.

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Pred. No. 2e-42;
0; Mismatches 417; Indels
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AAT42166 standard; DNA; 3319

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AAT42166 RESULT

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                                               gtccgagaacacccgtcgaccggcccctacgtggaggacttggcgaagctggtcgtgcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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11-JUL-2000;
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                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA
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                                                                                                                                                                                Claim 1; SEQ ID NO 1672; 21pp + Sequence Listing; English.
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Search completed: July 25, 2002, 05:44:40 Job time: 6948 sec

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228, Appl
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3, Appl
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                                                    Sequence 28, A Sequence 23, A Sequence 23, A Sequence 3, Ap Sequence 1, Ap Sequence 1, Ap Sequence 209, Sequence 10, Ap Sequence 10, Ap Sequence 11, Ap Sequence 17, Ap Sequence 17, Ap Sequence 209, Sequence 208, Ap Sequence
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Pred. No. 2.6e-103;
0; Mismatches 739;
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Patent No. 6013454

GENERAL INFORMATION

APPLICANT: Tang, Y. Tom

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

TITLE OF INVENTION: KIRESIN-LIKE MOTOR PROTEIN

FILE REFERENCE: PF-0593 US

CURRENT APPLICATION UNMERR: US/09/162,373

CURRENT FILING DATE: 1998-09-28

NUMBER: PERL PROGRAM

SOFTWARE: PERL PROGRAM
                                 US-09-541-782-1

US-08-468-036-28

US-08-468-036-23

US-08-376-843-23

US-09-723-153-3

US-09-721-383-3

US-09-721-383-1

US-08-78-183-1

US-08-78-183-1

US-08-78-183-1

US-08-78-183-1

US-08-181-891-209

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Best Local Similarity 55.0%;
Matches 1023; Conservative
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US-09-162-373-2
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Copyright (c) 1993 - 2000 Compugen Ltd
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APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Batterson, Chandra
TITLE OF INVENTION: KINESIN-LIKE MOTOR PROTEIN
FILE REFERENCE: PF-0593 US
CURRENT APPLICATION NUMBER: US/09/467,946
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/162,373
EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 3930
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Pred. No. 2.6e-103;
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US-09-467-946-2
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Matches 1023; Conservative
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US-09-467-946-2
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Best Local Similarity 55.8
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: 0. 6355471el motor pro-
TITLE OF INVENTION: their use
FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6355471el motor proteins and methods if
TITLE OF INVENTION: their use
TITLE REPRENCE: 1055
CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 264; DB 4; Length 107
55.9%; Pred. No. 7.6e-69;
Live 0; Mismatches 440; Indels
                                                                                                                                                                                                                                   Sequence 3, Application US/09722139 Patent No. 6355471
                                                    aactcgcgcagctga 1153
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Matches 604; Conservative
                                                                                                     1136 aaatagccagactga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-722-139-3
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LENGTH: 1077
                                                                                                                                                                                                             US-09-722-139-3
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                                                     aaatgccatgtgaaaccgtcagtaagatccacttggttgatcttgccggaagtgagcgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORD for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676B
FILING DATE: 15-JAN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08006676B Patent No. 5411865
GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Leishmania chagasi
US-08-006-676B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Oster, Jeffrey B.
REGISTRATION NUMBER: 32,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey B. Oster
STREET: 8339 SE 57th Street
CITY: Mercer Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 232 7845
TELERAX: (206) 236 0205
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                  57;
   Length 3319;
                                  Indels
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7.6%; Score 177.8; DB 1;
52.6%; Pred. No. 7.3e-43;
tive 0; Mismatches 417;
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                                  Conservative
                 Similarity
                                Matches 525;
 Query Match
Best Local S
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890 GGCGTGACGCCGCGGGATCTGCCCTGGAGATCTTTGCGCGGAAGGCGAGCGTGGAGGCGCAG 949
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Patent No. 5912166
GENERAL INFORMATION:
APPLICANT Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: LEISHMANIASIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1117 atgatccgcgagttgaaggaagtagcgcagctgagg 1155
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                                                                                                                  496 gacttgctgaatccgtcgacaaaggg
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-428-414A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3319;
                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: A 230Kd Antigen Present in Leishmania
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word for Macintosh Operating System 7.1 SOFTWARE: Microsoft Word for Macintosh 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 7.3e-43;
0; Mismatches 417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: PERKING, PATÍCIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
ITELEPHONE: 3310,614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                       Sequence 1, Application US/08282845
Patent No. 5719263
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacLitucsh
OPERATING SYSTEM: Apple Ma
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Best Local Similarity 52.6%;
Matches 525; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                               USA
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US-08-282-845-1
                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                  -08-282-845-1
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                                                                                         gogotagoggatatgtcgtc---gggaaaacagaagaagaatcagttagtaccttaccga
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TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia Anne
RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0444
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
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APPLICATION NUMBER: PCT/US94/00324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9400324 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex_Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania chaqasi
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,414A
FILING DATE: 21-APR-1995
CLASSIFICATION: 436
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                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kadlecek, Ann T.
REGISTRATION NUMBER: 39,244
REFERENCE/DOCKET NUMBER: 210121.407
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3319 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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3-09-718-841-1 Sequence 1, Application US/09718841

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Patent No. 6333184

GENERAL INFORMATION:

APPLICANT: Bereaud, Christophe
APPLICANT: Freedann, Richard
TITLE OF INVENTION: their use
FITLE OF INVENTION: their use
FILE REFERENCE: 1051
CURRENT APPLICATION NUMBER: US/09/718,841
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                            Length 1689;
                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 177.4; DB 4; Length 52.3%; Pred. No. 6.6e-43; tive 0; Mismatches 451; Indels
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; OTHER INFORMATION: n = a, t,
NAME/KEY: misc_feature
; LOCATION: (1171)...(1236)
; OTHER INFORMATION: n = a, t,
US-09-718-841-1
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.3
Matches 534; Conservative
                                                                                                                                                                                                                                             FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                1689
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ORGANISM: Caenorhabaditis elegans FEATURE:
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US-09-302-812-38/c
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                                                               865 cagaacteceaagtttteageagetgeeagageeteaacageteatettatateeeatae
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                                           gatatgtc------gtcgggaaaacagaagaagaatcagttagtaccttac
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Patent No. 633184

GENERAL INFORMATION:
APPLICANT: Bereadan, Richard
TITLE OF INVENTION: No. 6333184e1 motor proteins and methods for TITLE OF INVENTION: their use
TITLE TINVENTION: their use
TITLE REFERENCE: 1051
CURRENT APPLICATION NUMBER: US/09/718,841
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
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US-09-718-841-3
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Sequence 38, Application US/09302812B

Patent No. 6333148

GENERAL INFORMATION:
APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: LIN, Winston
TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG)
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACT
TITLE OF INVENTION: THEREWITH
FILE REFERENCE: NIAD 201
CURRENT APPLICATION NUMBER: 05/09/302,812B
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,768
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
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aatgaactgcagaaggacaagaacctcacttgcaccgtcgaagtttcgtacttggaaatt
                                             aaaga---ctgtgcctcactgccttcctctgtaggataaaagtaagttttctagaaatc
                                                                                        tacaatgaacgagtgcgagacttgctgaatccgtcgacaaaggggaa-----tctc
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17731 TCCCGAATIGGIGAAGACGGAGAAAGICATA---TIACAGIIGGICGACIAAAICIIGIA 17675
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                                    acaaacatgaacgagacatccagtcgatcccacgccgtcttcactttgaccttgacgcaa 711
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APPLICANT: Russell J. Stewart
TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
TITLE OF INVENTION: SEPARATIONS BY KINESINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Thorpe, No. 5830659th & Western, L.L.P.
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: AST Ascentia 900N OPERATING SYSTEM: DOS 6.22 SOFTWARE: Word Perfect 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/713,815A FILING DATE: 13.8EP-1996
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REFRENCE/DOCKET NUMBER: T321-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. HOWAITH
REGISTRATION NUMBER: 36,º
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3572 base pairs
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MEDIUM TYPE: Diskett
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US-08-713-815A-2
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CURRENT APPLICATION NUMBER: US/09/511,477

PRIOR APPLICATION NUMBER: 09/302,812

PRIOR FILING DATE: 1999-04-30
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                                                                    Length 29793;
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                                                               Score 118.2; DB 4;
Pred. No. 1.5e-24;
0; Mismatches 213;
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55.1%; Pred. No. 1.5e-24;
ive 0; Mismatches 213;
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APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: AME, Jean-Christophe
APPLICANT: LIN, Winston
                                                                  55.1%;
                                                             Query Match
Best Local Similarity 55.1;
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.1
Matches 287; Conservative
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US-09-302-812-38
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US-09-511-477-38
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                                                                 Length 3572;
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                                                                                        Indels
                                                                                      397;
                                                                 DB 2;
                                                                Score 107.8; DB 2
Pred. No. 5.8e-22;
0; Mismatches 397
                                                                 4.68;
                                                                 Query Match
Best Local Similarity 49.9
Matches 444; Conservative
TYPE: nucleic acid
STRANDEDNESS: double
                       linear
                      ; TOPOLOGY:
US-08-713-815A-2
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RESULT 14 US-09-572-191-5

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                                                                                                                                                                                                                                                                                                                                                                                          Length 1230;
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Sequence 5, Application US/09572191
Patent No. 6355466
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6355466el motor proteins and I
                                                                                                                                                                                                                                                                                                                                                                                      Score 106.4; DB 4;
Pred. No. 8.4e-22;
0; Mismatches 306;
                                                                                                                                                     FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                      4.5%;
ilarity 51.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 338; Conserv
                                                                                                                                                                                                                                                                                                          ) ORGANISM: Human
US-09-572-191-5
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4.5%; Score 106.4; DB 4; Length 4757;
Best Local Similarity 51.1%; Pred. No. 1.8e-21;
Matches 338; Conservative 0; Mismatches 306; Indels 18; Gaps
US-09-572-191-1

Sequence 1, Application US/09572191

Sequence 1, Application US/09572191

Sequence 1, Application US/09572191

APPLICANT: Beraud, Christophe

APPLICANT: Beraud, Christophe

APPLICANT: Sakowicz, Roman

APPLICANT: Wood, Kenneth

TITLE OF INVENTION: No. 6355466el motor proteins and methods for INTER REPERBNCE: 1017

CURRENT APPLICATION NUMBER: US/09/572,191

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 6

SOFTMARE: FastSEQ for Windows Version 1
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; ORGANISM: Human
US-09-572-191-1
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LENGTH: 4757
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1134

Search completed: July 25, 2002, 05:38:29 Job time: 6617 sec

222.4 9.5 507 9 AI339237 220.6 9.4 634 9 BBL64569 220.6 9.4 932 9 AI323149 220 9.4 1030 10 BM451369	22 216 9.2 588 9 AV594757 AV594757 AV594757 AV594757 AV594757 C 23 215.8 9.2 479 9 A1360405 A1360405 Gy85h09.x 24 213.2 9.1 561 10 BF150140 BF150140 UP82c07.y C 25 210.4 8.9 458 10 BF950986 BF950986 UT-M-BH4-26 27 208.4 8.9 456 9 AW125600 AW125600 UT-M-BH2.	207.6 8.8 588 9 AWB98094 206.6 8.8 646 9 AA097269 204 8.7 972 10 BW475082 202.8 8.6 423 9 AI323139 207 8.5 532 9 AI360260	32 200 6:3 532 5 MOUGO260 33 198.4 8.4 485 10 BEB61354 34 198 8.4 660 10 BE258249 35 197.2 8.4 457 10 RF348645	195 8.3 494 9 A1933167 193 8.2 799 10 BG393452 192 8.2 869 10 BE380022	39 190.2 8.1 443 9 AA097858 40 189.8 8.1 489 10 BF281801 41 189 8.0 560 10 BG920903	186.2 7.9 424 9 A4256792 185.8 7.9 585 10 BE887181 181.2 7.7 545 9 AW360994 177.8 7.6 417 9 BB733392	ALIGNMENTS	BC005977	DEFINITION Homo sapiens, Similar to kinesin family member 13B, clone IMAGE:4103715, mRNA. ACCESSION BC005977		SOURCE numan. ORGANISM Homo sapiens URGATYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1683)	AUTHORS STRUBBERGY,K.  TITLE Direct Submission JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office. National Cancer Tractities 31 Canter Daily Down 11003	REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov	Email: cgapbs-remail.nih.gov Tissue Procurement: ATC CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site:	<pre>Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.</pre>	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: d Column: 11    This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 8896163    This clone has the following problem: frame shifted.    Location/Qualifiers   Location/Q
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: July 25, 2002, 03:46:42; Search time 2969.55 Seconds (without alignments) 10690.117 Million cell updates/sec	Title: US-09-235-416-2 Perfect score: 2352 Sequence: 1 atgtcgggcggtggaaatataaacagcgaagcaggaattc 2352	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 13736207 seqs, 6748477542 residues  Total number of hits satisfying chosen parameters: 27472414	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Ĕ			10: gb_est2:* 11: gb_htc:* 13: gb_htc:*	12: 9D_98s: 13: em_gss_hum:* 14: em_gss_lnv:* 15: em_gss_pln:* 16: em_gss_vrt:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES QUEY	SCOLE MALCH Length DB 1D 321 13.6 1683 11 BC005977 277.4 11.8 1074 10 B1906040 277.2 11.8 670 9 AIR16019 270.2 11.5 1263 11 AK020905 264.4 11.2 694 10 B1281667	256.8 10.9 1014 256.4 10.9 770 255.6 10.9 853	10 255.2 10.9 774 10 EG473130 EG473131 11 236.8 10.1 670 9 AIB79422 AIB79422 12 233.4 9.9 594 9 AIS70691 AIS70691 14 226.4 9.6 586 10 BE252943 BE25294 15 225.8 9.6 670 10 BF468073 BF46807 16 224.6 9.5 690 10 BI685690 BI685690

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                                                                                                                                                 Length 1683;
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0; Mismatches 460;
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345 c 423 g 39
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58.1%;
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/issue_rype="leukcoyte"
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/lab.host="DHIOB"
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (ECORV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2.3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH.MGC Library."
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1 (bases 1 to 1074)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can idend through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1531 row. c column: 21
High quality sequence stop: 863.
Location/Qualifiers
                                                                                   AGTGCTGGCAA---AACAAGAATAAATTTGTTCCATATCGTGACTCAGTTCTCACTTGG
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                                            895 tcgtcgggaaaacagaagaagaatcagttagtaccttaccgagattcggtactgacgtgg
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Pred. No. 2.6e-63;
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/dev_stage="5 months post-conception"
/lab_host="NHON"
/note="Organ: brain; Vector: pBluescript SK (Stratagene);
Stle_1: Sstl; Site_2: Xno!; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
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Pred. No. 2.2e-63;
0; Mismatches 219;
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11.8%;
Best Local Similarity 65.7%;
Matches 437; Conservative
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

E Adachl,J., Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Sadachl,J., Alzawa,K., Ruhishl,Y., Furuno,M., Hanagaki,T.,
Carlinci,P., Fukuda,S., Fukunishl,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,M., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukwa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinaqawa,A., Takahashi,F.,
Tanaka,T., Tagami,M., Tagawa,A., Takahashi,F.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Further details.

CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Bncyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. First strand CDNA was primed with a primer [5, GAGAGAGAGAGACACTCTATTTTTTTTTTTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through two rounds of normalization to Rot = 20.0 and subtraction adapter of sequence [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama RIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Fax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="retina"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1263
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RIKEN full-length enriched library,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The RIKEN Genome Exploration Research Group Phase II Team and the
  99cccctacgtggaggacttggcgaagctggtcgtgcgatcattccaagaaatcgaaat 612
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HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult retina cDNA to mRNA, clone_lib.RIKEN full-length enriched mouse cDNA library clone:A930029L02.
Mus musculus
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clone:A930029L02:kinesin 13B, full insert sequence.
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High-efficiency full-length cDNA cloning
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/db_xref="taxon:10116"
/clone="U1-R-CTOS-cav-a-11-0-U1"
/clone_lb="U1-R-CTOS"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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Pred. No. 6.3e-60;
0; Mismatches 238;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                  39 AGGAAAATGAAGAACAGAGTTTTAAAGTCGAAGTGTCGTACATGGAAATTTATAATGAAA
                                                                                                                                                                                                                                                                                                                              GTGTGTTGGGACCCTACGTGGATGGACTTTCTAAACTGGCTGTCACAAGCTAAAAGGATA
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bp mRNA linear EST 05-FEB-2002
Homo sapiens cDNA clone IMAGE:5579159
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                       683 acgccgtcttcactttgaccttgacgcaaaagtggcatgatgaagagaccaaaatggaca
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                                                             DB 10;
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1350 row: m column: 12
High quality sequence start: 22
High quality sequence start: 22
Liccation/Qualifiers
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NHH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                       acatgaacgagacatccagtccgatcccacgccgtcttcactttgaccttgacgcaaaagt
                                                                      tggcgggttctgagcgagcaacgtccaccggagctactggagcgactgaaggaggtg
                                                                                                                                                                                     tccaagaaatcgaaaatctcatggatgagggcaacaaaggccagaacggttgccgccacaa
                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
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/ Organism="Homo sapiens"

/ Adb_xref="taxon:960s"

/ Adb_xref="taxon:960s"

/ Clone=lib="NIH_MGC_67"

/ Clone=lib="NIH_MGC_67"

/ Lab_host="DH100 {phage-resistant)"

/ Lab_host="DH100 {phage-resistant)"

/ Anote="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Library constructed by Liff

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9 a 214 c 228 g 256 t 7 others
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                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12335 row: f column: 24
High quality sequence stop: 583.
Location/Qualifiers
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Pred. No. 8.7e-58;
0; Mismatches 332; Indels
 Ph.D.
Contact: Robert Strausberg, E
Email: cgapbs-rêmail.nih.gov
Tissue Procurement: ATCC
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al Similarity 59.6%;
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COUNT Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1090 Std Error: 0.00
Seq primer: -400P from Gloco
High quality sequence stop: 407.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               AI363308 110-FEB-1999 9257c04.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016102 3' similar to SW:KF1A_HUMAN Q12756 KINESIN-LIKE PROTEIN KIF1A ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute / National institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gen
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Bonaldo, Ph.D.
                                      ----ttagtaccttaccgagattcggtactgacgtggcttctgaaggactccttgggagg
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                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2016102"
/clone=11b="NCI_CGAP_Brn23"
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/lab_host="DH108"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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BG473130 774 bp mRNA linear EST 21-MAR-2001 602515112F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4646835 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                    tttgccaggacatgttccggcgtattaatgaactgcagaaggacaagaacctcacttgca 451
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62.3%; Pred. No. 1.7e-57;
iive 0; Mismatches 254;
                                                                                                                                                                ¥
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/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
a 210 c 208 g 270
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                       Location/Qualifiers
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Mational Institute of Radiological Sciences
Anagawa 4-9-1, Inbo Chiba 263-8555, Japan
Email: kmita@hirs.go.jp
method:unl-directional sequence direction:sequenced from T3 primer
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                                                                                                                                      CNTACACAATGATGGGCAAGCAGGAGGACCAGCAGGGCCATCATCCCACAGCTCTGCG 510
                                                      284 atgcattcaagggttataaacaattgtatcttcgcctacggtcagaccggttcgggcaagt 343
                                                                       509 AGGACCICTCTCGGGATCAACGACGACGACGAC---ACANTGTCCTACTCCGTGG 453
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                                 Indels
  Score 256.4; DB 9;
Pred. No. 9.5e-58;
0; Mismatches 208;
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al Similarity 65.3%;
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E 1 (bases 1 to 774)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.lini.gov

Plate: LLCM1422 row: h column: 04

High quality sequence stop: 753.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='Inb="NIH_MGC_16"
/tissue_type="retinoblastoma"
/t
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A1879422 670 bp mRNA linear EST 23-AUG-1999 au50f08 x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518215 3' similar to SW:KF1A_HUMAN Q12756 KINESIN-LIKE A1879422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and 3' adaptor sequence:
5'-GAGAGAGACTCGAGTTTTTTTTTTTTTTTTTT"-3'. The library was
size-selected for >0.5 kb inserts and has an average
insert size estimated at 1.2 kb. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 670)
1 (bases I to 670)
1 (bases I. schola, N. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schollenberg, K., Steptoe, M., Tan, F., Theising, B., Washir, N., Mylie, T., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 423.
Location/Qualifiers
                                                                                                                                                                                                                                                      820
                                                                                                                                                                                                                                                                                                                                                                                                                ggttgccgccacaaacatgaacgagacatccagtcgatcccacgccgtcttcactttgac 701
                                                                                                                            761
                                                                                                                                                                                                                                                                                                                                                                            821 gactgaaggagggtgcagagatcaaccgctcactttcgaccctaggtcgtgtgattgcag 880
                                                                                                                      cagtotag-tagatttgggggttctgagcgagcaacgtccaccggagctactggagcgc
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Other_ESTS: aus0f08.y1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .670 "Acanism" Homo sapiens" "Ad_xxref"-taxon:9606" "Aclone="IMAGE:218215" "Clone="IMAGE:2518215" "Aclone=11b="Schneider fetal brain 00004"
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/dev_stage="5 months post-conception"
/lab_host="DH10B"
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358; Conservative
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constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Librar was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy). I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                 273 gcttctggataatgcattcaagggttataacaattgtatcttcgcctacggtcagaccgg 332
                                                                                                                                                                                                  ttcgggcaagtcctattcaatgatgggctatggcaaggagcat----ggcgtgatccc 386
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston

Bunmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I

(Dases 1 to 592)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                  ttgcaccgtcgaagtttcgtacttggaaatttacaatgaacgagtgcgagacttgctgaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agctactggagcgcgactgaaggaggtgcagagatcaaccgctcactttcgaccctagg
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                                                                                                      Length
                                                                                                                             Indels
                                                                                                   Score 236.8; DB 9;
Pred. No. 1.6e-52;
0; Mismatches 228;
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                                                                                                  Query Match 10.1%;
Best Local Similarity 63.4%;
Matches 413; Conservative
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BG297948
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                                                BASE COUNT
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/note="Organ: eye, Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 578.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 aggacaagaacctcacttgcaccgtcgaagtttcgtacttggaaatttacaatgaacgag
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                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4507905"
/tlone="lb="NIH_MGC_94"
/tissue_type="retina"
/lab_host="PHIOB (phage=resistant)"
/lab_host="PHIOB (phage=resistant)"
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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atctcatggutgagggcaacaaagccagaacggttgccgccacaaacatgaacgagacat
                                               1. 586
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TITLE
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

CLone distribution: NG-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/lmage/image.html

Insert Length: 770 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 293.
                              AIS70691 564 bp mRNA linear EST 14-APR-1999 tm79f05.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2164353 3' similar to SW:KF1A_HUMAN Q12756 KINESIN-LIKE PROTEIN KIF1A ;, mRNA
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                                                                                                                                                                                                                                                                                                                             Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                  1 (bases 1 to 564)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 aggacaagaacctcacttgcaccgtcgaagtttcgtacttggaaatttacaatgaacgag 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 CG---ACANACATGTCCTACTCCGTGNAGGTCAGCTACATGGAGAGATTACTGTGAGCGCG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgcgagacttgctgaatccgtcgacaaaggggaatctcaaggtccgagaacacccgtcga 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 agcatggcgtgatcccgcggatttgccaggacatgttccggcgtattaatgaactgcaga 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 233.2; DB 9; Length 564; 65.1%; Pred. No. 1.4e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 564
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                            sequence.
A1570691
A1570691.1 GI:4534065
                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 65.1
Matches 356; Conservative
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                                                                                                                                         human.
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586 bp mRNA linear EST 13-JUL-2000 mRNA sequence.
BES52943
EEST. 01:9123079
EST. 01:9123079
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Eukaryota Ito Sutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota Ito Sutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 580; The 1.010; Mathonal Institutes of Health, Mammalian Gene Collection (MGC)

Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMI66 row: c column: 09

High quality sequence stop: 586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
850
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                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                               791 gagcaacgtccaccggagctactggagcgcgactgaaggagggtgcagagatcaaccgct
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3388016"
/clone=lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B" (phage-resistant)"
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Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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UI-M-CDO-ayk-e-10-0-UI.rl NIH_BMAP_Ret2 Mus musculus cDNA clone
UI-M-CDO-8yk-e-10-0-UI 5', mRNA sequence.
                                                             acctcacttgcaccgtcgaagtttcgtacttggaaatttacaatgaacgagtgcgagact 499
                                                                                                                                        500 tgctgaatccgtcgacaaaggggaatctcaaggtccgagaacacccgtcgaccggccct 559
                                                                                                                                                                                                                                                                                                      atgagggcaacaaagccagaacggttgccgccacaaacatgaacgagacatccagtcgat 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaccggagctactggagcgcgactgaaggagggtgcagagtcaaccgctcactttcga 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CCTCAGGGGCCCGGGGCATGCGCCTGAAGGAAGGAGCCAACATCAATAAGTCCCTGACTA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccctaggtcgtgtgattgcagcgctagcggatatgtcgtcgggaaaacagaagaagaatc 919
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                                                                                                   AGCTATCCTACTCTGTGGAGGTGAGCTATATGGAGATCTACTGTGAGCGGGTACGAGACC 68
                                                                                                                                                                                                                         acgiggaggactiggcgaagciggicgigggatcaliccaagaaaicgaaatctcaigg
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                           3;
                           Indels
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National Institute of Mental Health
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97044477
      Pred. No.
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    63.18;
                     366; Conservative
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/strain="C578L/GB."
/db_xref="taxon:10090"
/clone="UT-M-CD0-ayk-e-10-0-UI"
/clone="UT-M-CD0-ayk-e-10-0-UI"
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/clone="Ib="NIH_BMAP_Ret2"
/dev_stage="1 day"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Ib-In to Train The polylinker: Site_1: NOT I: Site_2: Eco RI; The PNIH_BMAP_Ret2 library is derived from mouse neonatal retlna tissue. For a detailed description of the library from which this clone was derived, please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                           281 ataatgcattcaagggttataacaattgtatcttcgcctacggtcagaccggttcgggca 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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availability will be considered under appropriate and limited collaborative arrangements Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 CCAGGACTGTGGCAGCTACCAACATGAATGAGACAAGCAGCCGTTCTCACGCTGTGTCA
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Pred. No. 1.5e-49;
0; Mismatches 243;
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167 c 141 g 199 t
                                                                          /organism="Mus musculus"
                                           Location/Qualifiers
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